

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:15:55 ; Search time 30 Seconds
(without alignments)
579.659 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169
Sequence: 1 MEORGONAPASGARRKRRGP.....HLSSGKFMYLEGNADSAXS 411

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2167	99.9	411	3	US-09-329-633A-2
2	2167	99.9	411	4	US-09-079-029-1
3	2163	99.7	411	4	US-09-134-618-2
4	2160	99.6	411	4	US-10-039-785-3
5	2152	99.2	412	4	US-09-333-593A-2
6	2135.5	98.5	440	3	US-08-883-036A-2
7	2135.5	98.5	440	3	US-09-336-201-2
8	1610.5	74.3	350	4	US-09-134-618-6
9	1597	73.6	303	4	US-09-333-593A-2
10	1072	49.4	468	4	US-09-013-895A-4
11	1072	49.4	468	4	US-09-565-918-2
12	1072	49.4	468	4	US-09-448-868-2
13	1072	49.4	468	4	US-10-039-785-1
14	1061.5	48.9	467	3	US-09-086-483A-6
15	1061.5	48.9	467	3	US-09-580-212-6
16	996	45.9	424	4	US-09-333-593A-8
17	819.5	37.8	386	3	US-09-086-483A-2
18	819.5	37.8	386	4	US-09-580-212-2
19	819.5	37.8	386	4	US-10-039-785-4
20	811.5	37.4	386	4	US-09-130-491-6
21	522	24.1	234	4	US-09-130-491-12
22	463	21.3	368	2	US-08-651-579-2
23	398.5	18.4	299	3	US-09-153-927-3
24	398.5	18.4	299	4	US-09-134-618-4
25	398.5	18.4	299	4	US-10-039-785-2
26	379.5	17.5	259	3	US-09-006-353A-2
27	379.5	17.5	259	4	US-09-573-986-2

28	342	15.8	67	4	US-09-527-236A-26	Sequence 26, Appl
29	264.5	12.2	471	4	US-09-513-007-2	Sequence 2, Appl
30	262	12.1	51	3	US-08-883-036A-4	Sequence 4, Appl
31	262	12.1	51	4	US-09-536-201-4	Sequence 4, Appl
32	218	10.1	67	4	US-09-527-236A-25	Sequence 25, Appl
33	214	9.9	453	3	US-09-086-483A-5	Sequence 5, Appl
34	214	9.9	453	3	US-09-580-212-5	Sequence 5, Appl
35	210.5	9.7	455	1	US-08-050-319B-25	Sequence 25, Appl
36	210.5	9.7	455	1	US-08-321-668-2	Sequence 2, Appl
37	210.5	9.7	455	1	US-08-837-941-2	Sequence 2, Appl
38	210.5	9.7	455	2	US-08-126-016-2	Sequence 2, Appl
39	210.5	9.7	455	2	US-08-465-982-25	Sequence 25, Appl
40	210.5	9.7	455	3	US-08-815-469-5	Sequence 5, Appl
41	210.5	9.7	455	3	US-09-006-353A-3	Sequence 3, Appl
42	210.5	9.7	455	4	US-09-527-236A-5	Sequence 5, Appl
43	210.5	9.7	455	4	US-08-054-970-2	Sequence 2, Appl
44	210.5	9.7	455	4	US-09-565-918-4	Sequence 4, Appl
45	210.5	9.7	455	4	US-09-573-986-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-329-633A-2
Sequence 2, Application US/09329633A
Patent No. 6252050
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chundathapal, Anan
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
FILE REFERENCE: P14681 (REVISED)
CURRENT FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US/09/329, 633A
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: xaa
LOCATION: 410
OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2

Query Match 99.9% Score 2167, DB 3: Length 411;

Best Local Similarity 100.0%; Pred. No. 5.6e-198; Mismatches 0; Indels 0; Gaps 0;

Matches, 411: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MEORGONAPASGARRKRRGP...PRLRYPKTLVVAVALLVSAESALITQOD 60
|||||
1 MEORGONAPASGARRKRRGP...PRLRYPKTLVVAVALLVSAESALITQOD 60
61 LAPQORAPQOKRSSPSEGLCP...PGHHISEDRDCISCKYGGDYSTHMDLLFCLRTCD 120
|||||
61 LAPQORAPQOKRSSPSEGLCP...PGHHISEDRDCISCKYGGDYSTHMDLLFCLRTCD 120
61 LAPQORAPQOKRSSPSEGLCP...PGHHISEDRDCISCKYGGDYSTHMDLLFCLRTCD 120
121 SGEVELSPCTTRNTVCOCEGTREDS...PMCKRCRTGCGRGWVKVGDCTPMWDIECVH 180
|||||
121 SGEVELSPCTTRNTVCOCEGTREDS...PMCKRCRTGCGRGWVKVGDCTPMWDIECVH 180
121 SGEVELSPCTTRNTVCOCEGTREDS...PMCKRCRTGCGRGWVKVGDCTPMWDIECVH 180
181 KESGIITGVVAAVLVAVFVCKSLMK...KVLPLKIGISGGGDPERVDSSORPGAED 240
|||||
181 KESGIITGVVAAVLVAVFVCKSLMK...KVLPLKIGISGGGDPERVDSSORPGAED 240
181 KESGIITGVVAAVLVAVFVCKSLMK...KVLPLKIGISGGGDPERVDSSORPGAED 240
241 NVLNEIVSILOPTOVPEQEMVQEP...EPTGVNMLSPGESEHLLPEAEARSQRRLVPA 300
|||||
241 NVLNEIVSILOPTOVPEQEMVQEP...EPTGVNMLSPGESEHLLPEAEARSQRRLVPA 300
241 NVLNEIVSILOPTOVPEQEMVQEP...EPTGVNMLSPGESEHLLPEAEARSQRRLVPA 300

QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 2

US-09-079-029-1
Sequence 1, Application US/09079029
Patent No. 6342369

GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntcharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079, 029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maichang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-1

Query Match 99.9%; Score 2167; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 5,6e-198;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQGNAPASGARKRHGPGPREARGARPEGLRVKTLVVAVALLVSAESALITQOD 60
DB 1 MEQGNAPASGARKRHGPGPREARGARPEGLRVKTLVVAVALLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSGCLCPGHHISEDRDCISCKYGGDYSTHNNDLFLCRLCTRC 120
DB 61 LAPQORAPPOOKRSSPSGCLCPGHHISEDRDCISCKYGGDYSTHNNDLFLCRLCTRC 120
QY 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRCTGPRGAVKVGDCITPMSDIECVH 180
DB 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRCTGPRGAVKVGDCITPMSDIECVH 180
QY 181 KESGIIIGVYAAVVAVVAVCKSLMKKVLPLYLKGICSGGGDPERVDRSSORPGAED 240
DB 181 KESGIIIGVYAAVVAVVAVCKSLMKKVLPLYLKGICSGGGDPERVDRSSORPGAED 240
QY 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPAAERSSORRLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPAAERSSORRLVPA 300

QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 3

US-09-134-618-2
Sequence 2, Application US/09134618
Patent No. 6417328

GENERAL INFORMATION:
APPLICANT: Alnemri, Enad S.
TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
FILE REFERENCE: 480140.432
CURRENT APPLICATION NUMBER: US/09/134, 618
CURRENT FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-134-618-2

Query Match 99.7%; Score 2163; DB 4; Length 411;
Best Local Similarity 99.5%; Pred. No. 1,4e-197;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQGNAPASGARKRHGPGPREARGARPEGLRVKTLVVAVALLVSAESALITQOD 60
DB 1 MEQGNAPASGARKRHGPGPREARGARPEGLRVKTLVVAVALLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSGCLCPGHHISEDRDCISCKYGGDYSTHNNDLFLCRLCTRC 120
DB 61 LAPQORAPPOOKRSSPSGCLCPGHHISEDRDCISCKYGGDYSTHNNDLFLCRLCTRC 120
QY 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRCTGPRGAVKVGDCITPMSDIECVH 180
DB 121 SGEVELSPCTTTNTVCCCEGTFRREDSPEMCRKCRCTGPRGAVKVGDCITPMSDIECVH 180
QY 181 KESGIIIGVYAAVVAVVAVCKSLMKKVLPLYLKGICSGGGDPERVDRSSORPGAED 240
DB 181 KESGIIIGVYAAVVAVVAVCKSLMKKVLPLYLKGICSGGGDPERVDRSSORPGAED 240
QY 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPAAERSSORRLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPAAERSSORRLVPA 300
QY 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
DB 301 NEGPTETLRCCFDDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETTLGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 4

US-10-039-785-3
Sequence 3, Application US/10039785
Patent No. 6538938

GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039, 785
CURRENT FILING DATE: 2002-05-07

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: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
: PRIOR APPLICATION NUMBER: 60/341,237
: PRIOR FILING DATE: 2001-12-20
: PRIOR APPLICATION NUMBER: 60/331,310
: PRIOR FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/331,044
: PRIOR FILING DATE: 2001-11-07
: PRIOR APPLICATION NUMBER: 60/327,364
: PRIOR FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: 60/323,807
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/309,176
: PRIOR FILING DATE: 2001-08-02
: PRIOR APPLICATION NUMBER: 60/294,981
: PRIOR FILING DATE: 2001-06-04
: PRIOR APPLICATION NUMBER: 60/293,473
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-039-785-3

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Query Match      99.6%; Score 2160; DB 4; Length 411;
Best Local Similarity 99.3%; Pred. No. 2,6e-197;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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D 1 MEORGNAPASGARKRHGPGPREARGARGLRVPKTLVVAALLVSAESALITQOD 60
QY 61 LAPQRAAPQOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNDLLFCLRCTCD 120
D 61 LAPQRAAPQOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
D 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
QY 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERRVDRSSORPAED 240
D 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERRVDRSSORPAED 240
QY 241 NVLNEIVSILOPTQVPEQMEVQEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
D 241 NVLNEIVSILOPTQVPEQMEVQEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
QY 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMNDIEIKVAKAEAGHRDTLYTMLIKW 360
D 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMNDIEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411
D 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411

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RESULT 5
US-09-333-593A-2
: Sequence 2, Application US/09333593A
: Patent No. 6133269
: GENERAL INFORMATION:
: APPLICANT: DEEN, KEITH C.
: APPLICANT: YOUNG, PETER R.
: APPLICANT: MARSHALL, LISA A.
: APPLICANT: ROSHAK, AMY K.
: APPLICANT: TAN, KONG B.
: APPLICANT: TRUENH, ALEMSEGED
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
: CURRENT APPLICATION DATA: TR6
: FILING DATE: GH-50008-2

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: CURRENT APPLICATION NUMBER: US/09/333,593A
: CURRENT FILING DATE: 1999-06-15
: PRIOR APPLICATION NUMBER: 08/916,625
: PRIOR FILING DATE: 1997-08-22
: PRIOR APPLICATION NUMBER: 08/853,684
: PRIOR FILING DATE: 1997-05-09
: PRIOR APPLICATION NUMBER: 60/041,230
: PRIOR FILING DATE: 1997-03-14
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 412
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-333-593A-2

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Query Match      99.2%; Score 2152; DB 4; Length 412;
Best Local Similarity 99.3%; Pred. No. 1.5e-196;
Matches 408; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MEORGNAPASGARKRHGPGPREARGARGLRVPKTLVVAALLVSAESALITQOD 60
D 1 MEORGNAPASGARKRHGPGPREARGARGLRVPKTLVVAALLVSAESALITQOD 60
QY 61 LAPQRAAPQOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNDLLFCLRCTCD 120
D 61 LAPQRAAPQOKRSSPSEGLCPRGHHSSEGRDCISCKYGODYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
D 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCKKCTGCRGVKVGDDCTPMSDIECVH 180
QY 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERRVDRSSORPAED 240
D 181 KESGIIIGVYAAVLLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERRVDRSSORPAED 240
QY 241 NVLNEIVSILOPTQVPEQMEVQEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
D 241 NVLNEIVSILOPTQVPEQMEVQEPAPPTGVNMLSPGESEHLLPAPAEERSQRRLLVPA 300
QY 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMNDIEIKVAKAEAGHRDTLYTMLIKW 360
D 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMNDIEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411
D 361 VNKTGRDASVHTLLDALETIGERLAKOKIEDHLSSGKFMYLEGNADSAMS 411

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RESULT 6
US-08-883-036A-2
: Sequence 2, Application US/08883036A
: Patent No. 6072047
: GENERAL INFORMATION:
: APPLICANT: Rauch, Charles
: APPLICANT: Malczak, Henning
: TITLE OF INVENTION: Receptor That Binds TRAIL
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle,
: STATE: WA
: COUNTRY: US
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: Apple Power Macintosh
: SOFTWARE: Microsoft Word, Version 6.0.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/883,036A
: FILING DATE: 26-JUN-1997

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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --to be assigned--
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/815,255
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/799,861
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2625-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-883-036A-2

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Query Match          98.5%; Score 2135.5; DB 3; Length 440;
Best Local Similarity 93.0%; Pred. No. 6.2e-195;
Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

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QY 1 MEQKGNAPASGARKRHGPGPREARARGLRVPKTLVVAVLLVSAESALITQOD 60
DB 1 MEQKGNAPASGARKRHGPGPREARARGLRVPKTLVVAVLLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSSEGLCPGPHHISEDGRDCISCKYGODYSTHWNDLFCRLCTRC 120
DB 61 LAPQORAPPOOKRSSPSSEGLCPGPHHISEDGRDCISCKYGODYSTHWNDLFCRLCTRC 120
QY 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCRKCRGCGRWKVGDDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCRKCRGCGRWKVGDDCTPMSDIECVH 180
QY 181 KE-----SGIIIGTVAAVLLIYAVFCKSLMKKV 211
DB 181 KESGTHSGEAPAVEETVTSPPGPASPCLSGIIIGTVAAVLLIYAVFCKSLMKKV 240
QY 212 LPYLKIGISGGGGPERVDRSSQRPAGADNVNLNETIVSILQPTQVPEQEMEYQEPAEPTGV 271
DB 241 LPYLKIGISGGGGPERVDRSSQRPAGADNVNLNETIVSILQPTQVPEQEMEYQEPAEPTGV 300
QY 272 NMLSPGSEHLLPEAEERSQRRLLVANEGDPTETLRQCFDFADLVPPDSMEPLMKR 331
DB 301 NMLSPGSEHLLPEAEERSQRRLLVANEGDPTETLRQCFDFADLVPPDSMEPLMKR 360
QY 332 LGLMDNETKVAKAAGHRTLYTMLIKWVKTKGRDASVHTLLDALETLGRLAKOKIED 391
DB 361 LGLMDNETKVAKAAGHRTLYTMLIKWVKTKGRDASVHTLLDALETLGRLAKOKIED 420
QY 392 HLSSGKFMYLEGNADSAXS 411
DB 421 HLSSGKFMYLEGNADSAXS 440

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RESULT 7
US-09-536-201-2
Sequence 2, Application us/09536201
Patent No. 6569642
GENERAL INFORMATION:
APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning

```

```

TITLE OF INVENTION: Receptor That Binds TRAIL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle,
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,201
FILING DATE: 27-MAR-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/883,036
FILING DATE: 26-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --to be assigned--
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/815,255
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/799,861
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2625-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-536-201-2

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Query Match          98.5%; Score 2135.5; DB 4; Length 440;
Best Local Similarity 93.0%; Pred. No. 6.2e-195;
Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

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QY 1 MEQKGNAPASGARKRHGPGPREARARGLRVPKTLVVAVLLVSAESALITQOD 60
DB 1 MEQKGNAPASGARKRHGPGPREARARGLRVPKTLVVAVLLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSSPSSEGLCPGPHHISEDGRDCISCKYGODYSTHWNDLFCRLCTRC 120
DB 61 LAPQORAPPOOKRSSPSSEGLCPGPHHISEDGRDCISCKYGODYSTHWNDLFCRLCTRC 120
QY 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCRKCRGCGRWKVGDDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTREEDSPCMCRKCRGCGRWKVGDDCTPMSDIECVH 180
QY 181 KE-----SGIIIGTVAAVLLIYAVFCKSLMKKV 211
DB 181 KESGTHSGEAPAVEETVTSPPGPASPCLSGIIIGTVAAVLLIYAVFCKSLMKKV 240
QY 212 LPYLKIGISGGGGPERVDRSSQRPAGADNVNLNETIVSILQPTQVPEQEMEYQEPAEPTGV 271
DB 241 LPYLKIGISGGGGPERVDRSSQRPAGADNVNLNETIVSILQPTQVPEQEMEYQEPAEPTGV 300

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STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,895A
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEF, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
FAX: (202) 371-2340
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-895A-2

Query Match          49.4%; Score 1072; DB 4; Length 468;
Best Local Similarity 54.8%; Pred. No. 1.2e-93;
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GONAPASGARRKRGPGREARGARPGRLVPRKTLVLAVAL-LVSAESALITQODLAP 63
DB 60 GONHPSAR-ARAGRAPRPARPARASPRLRVHKTEFVYVGLQVPPSSATIKLHD--- 115
QY 64 QORAPQOKRSSPBGCLCPGHHISEGDRDCISCKYGODYSTHNDLLFCLRCTRCSGSE 123
DB 116 -QSIGTOQWHSPLGELCPGSHRSERPGACNCTEGVYTNASNLFACLPCTACKSDE 174
QY 124 VELSPCTTRNTVOCCEGTFREDSPGCRKCRGCGRWVKGDDCTPMSDIECVHES 183
DB 175 EERSPCTTRNTACQCKGTFRNDNSAEMCKKSTGCRGAVKXKDCIPMSDIECVHES 234
QY 184 G-----IIGVTAVALVLAFAVCKSLMKKVLPLYLGIC---SGGGGDPERRVRS 233
DB 235 GNGHNIWILVTLVPLVLAVALI-----VCCIGSGCGGDPKMDRYC 279
QY 234 -----ORPAEDNVLEIYSILO--PTQVPEQEMEQEPAEPTGVNMLSPGSEHLL 284
DB 280 FWRGLGLRPGAEENAHNELISNADSLSTFVSEQOMESQEPADLTGVVOSPGEAQCLLG 339
QY 285 PAEARSQRRRLVPAANGDPTETLRQCFDDFADLVPPDSWEPLMRKLGMDNEIKYAKA 344
DB 340 PAEAGSQRRLVPAANGADPTETLMLEFDKFAINIVPPDSMDQLMRDLTKNEIDVYRA 399
QY 345 EAAGHRDTLYTMLIKWVKTRGRDASVHTLDALETGRLAKOKIEDHLLSGKFMYLEG 404
DB 400 GTAGPGDALYMLKWKVTKGRNASIHTLLDALEMERHAKKIKQDLLVDSGKFIYED 459
QY 405 NADSAXS 411
DB 460 GTGSAYS 466
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RESULT 11
US-09-565-918-2

Sequence 2, Application US/09565918
Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.

```
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 2
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-2

Query Match          49.4%; Score 1072; DB 4; Length 468;
Best Local Similarity 54.8%; Pred. No. 1.2e-93;
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

QY 5 GONAPASGARRKRGPGREARGARPGRLVPRKTLVLAVAL-LVSAESALITQODLAP 63
DB 60 GONHPSAR-ARAGRAPRPARPARASPRLRVHKTEFVYVGLQVPPSSATIKLHD--- 115
QY 64 QORAPQOKRSSPBGCLCPGHHISEGDRDCISCKYGODYSTHNDLLFCLRCTRCSGSE 123
DB 116 -QSIGTOQWHSPLGELCPGSHRSERPGACNCTEGVYTNASNLFACLPCTACKSDE 174
QY 124 VELSPCTTRNTVOCCEGTFREDSPGCRKCRGCGRWVKGDDCTPMSDIECVHES 183
DB 175 EERSPCTTRNTACQCKGTFRNDNSAEMCKKSTGCRGAVKXKDCIPMSDIECVHES 234
QY 184 G-----IIGVTAVALVLAFAVCKSLMKKVLPLYLGIC---SGGGGDPERRVRS 233
DB 235 GNGHNIWILVTLVPLVLAVALI-----VCCIGSGCGGDPKMDRYC 279
QY 234 -----ORPAEDNVLEIYSILO--PTQVPEQEMEQEPAEPTGVNMLSPGSEHLL 284
DB 280 FWRGLGLRPGAEENAHNELISNADSLSTFVSEQOMESQEPADLTGVVOSPGEAQCLLG 339
QY 285 PAEARSQRRRLVPAANGDPTETLRQCFDDFADLVPPDSWEPLMRKLGMDNEIKYAKA 344
DB 340 PAEAGSQRRLVPAANGADPTETLMLEFDKFAINIVPPDSMDQLMRDLTKNEIDVYRA 399
QY 345 EAAGHRDTLYTMLIKWVKTRGRDASVHTLDALETGRLAKOKIEDHLLSGKFMYLEG 404
DB 400 GTAGPGDALYMLKWKVTKGRNASIHTLLDALEMERHAKKIKQDLLVDSGKFIYED 459
QY 405 NADSAXS 411
DB 460 GTGSAYS 466
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RESULT 12

US-09-448-868-2
Sequence 2, Application US/09448868
Patent No. 6461823

GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
TITLE OF INVENTION: Receptor 4). Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2540
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-448-868-2

Query Match 49.48; Score 1072; DB 4; Length 468;
Best Local Similarity 54.88; Pred. No. 1.2e-93;
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

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QY 5 GQNPASGARKRPGPREARPGRLVPTLVVAAYLL-LVSAESALITQODLAP 63
DB 60 GQHPSPAR-ARAGAPGPBPAPREASPRLRVHKTFKFFVVGVLQVPPSSAATIKLHD-- 115
QY 64 QQRAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNDLFLCRLCTRCSGE 123
DB 116 -QSTGTQOWEHSPLGELCPGSHRSERPGACNCTEGVGTNNASNNLFACLPCTACKSDE 174
QY 124 VELSPCTTTRNTVQCCEGTFREEDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVHKS 183
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKRCSTGCPRGWKVKDCTPMSDIECVHKS 234
QY 184 G-----IIGVTAAYVAVLVAVFVCKSLMKKVLPLYKIGC-----SGGGDPPERVDRSS 233
DB 235 GNGHNIVVILVTVLVPLLVAVLI-----VCCIGSGGGGDPKCMDBVC 279
QY 234 -----QRPAGEENVLEIYSILO--PTQVPEQEMEVOEAPETGVNMLSPGESEHLE 284
DB 280 FWRIGLGRGPAEDENAHNEIISNADSLSTFVSEQOMESQEPADLTGTVVOSPGAQCLLG 339
QY 285 PAEARSQORRLVLPANEGDPTETLRQCFDFAVLFPDSDPEMLRKLGLMDNEIKYAKA 344
DB 340 PAEAGSQORRLVLPANGADPTETLMLEFDFKFAIVFPDSDQMLRQDLTKNEIDIVRA 399
QY 345 EAAGHRTLVYMLTKWVNTKGRDASVHTLLDALETIGERLAKOKTIEDHLLSGKFMYLEG 404
DB 400 GTAGPGDALYAMLKWKVNTKGRNASIHTLLDALEMERERAKKEXIQLDLVDSGKFYLED 459
QY 405 NADSAXS 411
DB 460 GTGSAYS 466
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RESULT 13
US-10-039-785-1

Sequence 1, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PE550
CURRENT APPLICATION NUMBER: US/10/039,785
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-1

Query Match 49.48; Score 1072; DB 4; Length 468;
Best Local Similarity 54.88; Pred. No. 1.2e-93;
Matches 234; Conservative 39; Mismatches 114; Indels 40; Gaps 8;

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QY 5 GQNPASGARKRPGPREARPGRLVPTLVVAAYLL-LVSAESALITQODLAP 63
DB 60 GQHPSPAR-ARAGAPGPBPAPREASPRLRVHKTFKFFVVGVLQVPPSSAATIKLHD-- 115
QY 64 QQRAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNDLFLCRLCTRCSGE 123
DB 116 -QSTGTQOWEHSPLGELCPGSHRSERPGACNCTEGVGTNNASNNLFACLPCTACKSDE 174
QY 124 VELSPCTTTRNTVQCCEGTFREEDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVHKS 183
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKRCSTGCPRGWKVKDCTPMSDIECVHKS 234
QY 184 G-----IIGVTAAYVAVLVAVFVCKSLMKKVLPLYKIGC-----SGGGDPPERVDRSS 233
DB 235 GNGHNIVVILVTVLVPLLVAVLI-----VCCIGSGGGGDPKCMDBVC 279
QY 234 -----QRPAGEENVLEIYSILO--PTQVPEQEMEVOEAPETGVNMLSPGESEHLE 284
DB 280 FWRIGLGRGPAEDENAHNEIISNADSLSTFVSEQOMESQEPADLTGTVVOSPGAQCLLG 339
QY 285 PAEARSQORRLVLPANEGDPTETLRQCFDFAVLFPDSDPEMLRKLGLMDNEIKYAKA 344
DB 340 PAEAGSQORRLVLPANGADPTETLMLEFDFKFAIVFPDSDQMLRQDLTKNEIDIVRA 399
QY 345 EAAGHRTLVYMLTKWVNTKGRDASVHTLLDALETIGERLAKOKTIEDHLLSGKFMYLEG 404
DB 400 GTAGPGDALYAMLKWKVNTKGRNASIHTLLDALEMERERAKKEXIQLDLVDSGKFYLED 459
QY 405 NADSAXS 411
DB 460 GTGSAYS 466
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RESULT 14

US-09-086-483A-6
Sequence 6, Application US/09086483A
Patent No. 6214580
GENERAL INFORMATION:
APPLICANT: NI, et al.
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,483A
FILING DATE: May-29-98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,936
FILING DATE: May-30-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/069,112
FILING DATE: Dec-9-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PP379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8439
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-086-483A-6

Query Match 48.9%; Score 1061.5; DB 3; Length 467;
Best Local Similarity 54.8%; Pred. No. 1.2e-92;
Matches 234; Conservative 39; Mismatches 113; Indels 41; Gaps 9;

QY 5 GONAPASGARKRRGPGPREARGARPGLRVPKTLVLVAAYLL-LVSAESALLTQODLAP 63
DB 60 GQHPSPAR-ARAGRAPGPRAPRARESPRLRVHKTFRFVYGVLLVPPSSAATIKLHD-- 115

QY 64 QORAPPOOKRSSPSEGLCPGPHNISPDGRDCISCKYGQDYSTHNDLLFLCTRCDSGE 123
DB 116 -QSIGTQOWHESEFGLGELCPGSHRSERPGACNCRCTEGVGTNASNINLFLACLPCTACKSDE 174

QY 124 VELSPCTTTRNTVQCCEEGTFRREDSPBCKCKRTGCGPRGKAVKGDCTPMSDIECVHKS 183
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKKSTGCPRGWKVKDCTPMSDIECVHKS 234

QY 184 G-----IIGVTAAYVAVLVAVFVCKSLMKKVLPLKGC-----SGGGDPERVDRSS 233
DB 235 GNGHNINIVLVTLVLPVLLVAAYLI-----VCCIGSGCGGDPKCMRVC 279

QY 234 -----ORPGAEDNVINEIVSIQ--PTQVPEQEMEVOEPAEPTGVNMLSPGSEHLE 284
DB 280 FWRGLGRGAEEDNAINNELISNADSLSTFVSEQOMESQEPADLTGV-VQSPGEAQCCLLG 338

QY 285 PAEERSQRRRLVLANEGDPTETLLKQCFDDFADLVFPDSWEPLMRKLGMDNEIKYAKA 344
DB 285 PAEERSQRRRLVLANEGDPTETLLKQCFDDFADLVFPDSWEPLMRKLGMDNEIKYAKA 344

DB 339 PAEAGSORRRLVLANGADPTETLLMLFDFKFNANIVFPDSWQDLMRQDLITKNEIDVRA 398
QY 345 EAAGRPDLVNLMLKWNKGRDASVHTLLDALTEGLERAKOKIEPHLLSSGKFWLLEG 404
DB 399 GTAGPGDALYANMLKWNKGRNASIHTLLDALTEGMEERAKKEXIQLDLVDSGKFITYLED 458

QY 405 NADSAXS 411
DB 459 GTGSAXS 465

RESULT 15
US-09-580-212-6
Sequence 6, Application US/09580212
Patent No. 6506569
GENERAL INFORMATION:
APPLICANT: NI, Jian et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR10
FILE REFERENCE: PP379P1
CURRENT APPLICATION NUMBER: US/09/580,212
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/136,786
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/142,563
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/144,023
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 467
TYPE: PRT
ORGANISM: Homo sapiens
US-09-580-212-6

Query Match 48.9%; Score 1061.5; DB 4; Length 467;
Best Local Similarity 54.8%; Pred. No. 1.2e-92;
Matches 234; Conservative 39; Mismatches 113; Indels 41; Gaps 9;

QY 5 GONAPASGARKRRGPGPREARGARPGLRVPKTLVLVAAYLL-LVSAESALLTQODLAP 63
DB 60 GQHPSPAR-ARAGRAPGPRAPRARESPRLRVHKTFRFVYGVLLVPPSSAATIKLHD-- 115

QY 64 QORAPPOOKRSSPSEGLCPGPHNISPDGRDCISCKYGQDYSTHNDLLFLCTRCDSGE 123
DB 116 -QSIGTQOWHESEFGLGELCPGSHRSERPGACNCRCTEGVGTNASNINLFLACLPCTACKSDE 174

QY 124 VELSPCTTTRNTVQCCEEGTFRREDSPBCKCKRTGCGPRGKAVKGDCTPMSDIECVHKS 183
DB 175 EERSPCTTTRNTACQCKPGTFRNDNSAEMCKKSTGCPRGWKVKDCTPMSDIECVHKS 234

QY 184 G-----IIGVTAAYVAVLVAVFVCKSLMKKVLPLKGC-----SGGGDPERVDRSS 233
DB 235 GNGHNINIVLVTLVLPVLLVAAYLI-----VCCIGSGCGGDPKCMRVC 279

QY 234 -----ORPGAEDNVINEIVSIQ--PTQVPEQEMEVOEPAEPTGVNMLSPGSEHLE 284
DB 280 FWRGLGRGAEEDNAINNELISNADSLSTFVSEQOMESQEPADLTGV-VQSPGEAQCCLLG 338

QY 285 PAEERSQRRRLVLANEGDPTETLLKQCFDDFADLVFPDSWEPLMRKLGMDNEIKYAKA 344
DB 339 PAEAGSORRRLVLANGADPTETLLMLFDFKFNANIVFPDSWQDLMRQDLITKNEIDVRA 398

QY 345 EAAGRPDLVNLMLKWNKGRDASVHTLLDALTEGLERAKOKIEPHLLSSGKFWLLEG 404
DB 399 GTAGPGDALYANMLKWNKGRNASIHTLLDALTEGMEERAKKEXIQLDLVDSGKFITYLED 458

QY 405 NADSAXS 411
DB 459 GTGSAXS 465

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us-10-052-798-1.rai

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:19:51 ; Search time 52 Seconds

(without alignments)
938.659 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169
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Scoring table: BLUSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 segs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubppa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	2167	99.9	411	10	US-09-811-088-6
5	2167	99.9	411	10	US-09-892-964-11
6	2167	99.9	411	14	US-10-052-798-1
7	2167	99.9	411	15	US-10-207-655-194
8	2167	99.9	411	15	US-10-314-410-6
9	2163	99.7	411	14	US-10-067-615-2
10	2163	99.7	411	14	US-10-076-754-2
11	2163	99.7	411	14	US-10-076-773-2
12	2160	99.6	411	9	US-09-874-138-2
13	2160	99.6	411	13	US-10-039-785-3
14	2160	99.6	411	13	US-10-005-842-2
15	2152	99.2	411	8	US-08-916-625B-2

16	2133.5	98.4	440	9	US-09-757-421-2	Sequence 2, Appl1
17	2133.5	98.4	440	10	US-09-811-088-4	Sequence 4, Appl1
18	2133.5	98.4	440	15	US-10-314-410-4	Sequence 4, Appl1
19	1610.5	74.3	350	14	US-10-067-615-6	Sequence 6, Appl1
20	1610.5	74.3	350	14	US-10-076-754-6	Sequence 6, Appl1
21	1610.5	74.3	350	14	US-10-076-773-6	Sequence 6, Appl1
22	1597	73.6	303	8	US-08-916-625B-4	Sequence 4, Appl1
23	1072	49.4	468	13	US-10-039-785-1	Sequence 1, Appl1
24	1072	49.4	468	15	US-10-226-296-2	Sequence 2, Appl1
25	1072	49.4	468	15	US-10-226-318-2	Sequence 2, Appl1
26	1072	49.4	468	15	US-10-175-902-2	Sequence 2, Appl1
27	1065	49.1	418	10	US-09-887-879-14	Sequence 14, Appl1
28	1065	49.1	418	10	US-09-992-964-14	Sequence 14, Appl1
29	819.5	37.8	386	13	US-10-039-785-4	Sequence 4, Appl1
30	819.5	37.8	386	15	US-10-066-500-29	Sequence 29, Appl1
31	819.5	37.8	386	15	US-10-028-072-340	Sequence 340, App
32	819.5	37.8	386	15	US-10-121-049-340	Sequence 340, App
33	819.5	37.8	386	15	US-10-123-904-340	Sequence 340, App
34	819.5	37.8	386	15	US-10-140-470-340	Sequence 340, App
35	819.5	37.8	386	15	US-10-175-746-340	Sequence 340, App
36	819.5	37.8	386	15	US-10-176-918-340	Sequence 340, App
37	819.5	37.8	386	15	US-10-176-921-340	Sequence 340, App
38	819.5	37.8	386	15	US-10-002-796-29	Sequence 29, Appl1
39	819.5	37.8	386	15	US-10-066-494-29	Sequence 29, Appl1
40	819.5	37.8	386	15	US-10-066-494-29	Sequence 29, Appl1
41	819.5	37.8	386	15	US-10-137-865-340	Sequence 340, App
42	819.5	37.8	386	15	US-10-140-471-340	Sequence 340, App
43	819.5	37.8	386	15	US-10-142-431-340	Sequence 340, App
44	819.5	37.8	386	15	US-10-143-114-340	Sequence 340, App
45	819.5	37.8	386	15	US-10-140-002-340	Sequence 340, App

ALIGNMENTS

RESULT 1
US-09-828-739-2
Sequence 2, Application US/09828739
Patent No. US20020004227A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chantcharapai, Anan
APPLICANT: Kim, K. Jin
TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
FILE REFERENCE: P1468R1 (REVISED)
CURRENT APPLICATION NUMBER: US/09/828,739
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/329,633
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/089,253
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: human
FEATURE:
NAME/KEY: xaa
LOCATION: 410
OTHER INFORMATION: xaa - leu or met
US-09-828-739-2
Query Match 99.9%; Score 2167; DB 9; Length 411;
Best local Similarity 100.0%; Pred. No. 8e-187;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORGONAPASGARRKRRGPPRRARARGLRPRKTLVLYVAVALVLSAESALITQOD 60
|||||
DB 1 MEORGONAPASGARRKRRGPPRRARARGLRPRKTLVLYVAVALVLSAESALITQOD 60
|||||
QY 61 LAPQRAAPQQRSSPSGLCPGHHTISEDRDISCYGODYTHWNNDLFCRCRCD 120
|||||

Db 61 LAPQRAAPQOKRSSPSEGLCPGGHHSSEDRDICSCKYGQDYSTHWNDLFLCRLCTCD 120
QY 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240
Db 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240
QY 241 NVLNEIVSILOPTVOPQEMEVOPAPPTGVNMLSPGESEHLLLEPAERSSQRRLLVPA 300
Db 241 NVLNEIVSILOPTVOPQEMEVOPAPPTGVNMLSPGESEHLLLEPAERSSQRRLLVPA 300
QY 301 NEGDPTETLRCFCFDFADLVFPDSMEPLMRKLGIMDEIKAKAEAGHRTLYTMLIKW 360
Db 301 NEGDPTETLRCFCFDFADLVFPDSMEPLMRKLGIMDEIKAKAEAGHRTLYTMLIKW 360
QY 361 VNKTRDASVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411
Db 361 VNKTRDASVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411

RESULT 2

US-09-757-421-4
Sequence 4, Application US/09757421
Patent No. US20020048785A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: NOVEL POLYPEPTIDES WITHIN
THE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY AND
USES THEREFOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/757,421
FILING DATE: 10-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,652
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Melkiohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-757-421-4

Query Match 99.9%; Score 2167; DB 9; Length 411;
Best Local Similarity 99.8%; Pred. No. 8e-187;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEORGONAPASGARRKHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60

Db 1 MEORGONAPASGARRKHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60
QY 61 LAPQRAAPQOKRSSPSEGLCPGGHHSSEDRDICSCKYGQDYSTHWNDLFLCRLCTCD 120
Db 61 LAPQRAAPQOKRSSPSEGLCPGGHHSSEDRDICSCKYGQDYSTHWNDLFLCRLCTCD 120
QY 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240
Db 181 KESGIIIGVVAAVVLLVAVFVCKSLMKKVLPLYKIGICSGGGDPERVDRSSQRPGEAD 240
QY 241 NVLNEIVSILOPTVOPQEMEVOPAPPTGVNMLSPGESEHLLLEPAERSSQRRLLVPA 300
Db 241 NVLNEIVSILOPTVOPQEMEVOPAPPTGVNMLSPGESEHLLLEPAERSSQRRLLVPA 300
QY 301 NEGDPTETLRCFCFDFADLVFPDSMEPLMRKLGIMDEIKAKAEAGHRTLYTMLIKW 360
Db 301 NEGDPTETLRCFCFDFADLVFPDSMEPLMRKLGIMDEIKAKAEAGHRTLYTMLIKW 360
QY 361 VNKTRDASVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411
Db 361 VNKTRDASVHTLLDALETTGERLAKOKIEDHLLSSGKFMYLEGNDASXS 411

RESULT 3

US-09-887-879-11
Sequence 11, Application US/09887879
Patent No. US20020102706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Chantharapai, Anan
APPLICANT: Gurney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
TITLE OF INVENTION: APO-2/DR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/09/887,879
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 09/096,500
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/049,911
PRIOR FILING DATE: 1997-06-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 11
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Unsure
LOCATION: 410
OTHER INFORMATION: Xaa may be leucine or methionine
US-09-887-879-11

Query Match 99.9%; Score 2167; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 8e-187;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORGONAPASGARRKHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60
Db 1 MEORGONAPASGARRKHGPGPREARGARGLRVPTLVVAAVLLVSAESALITQOD 60
QY 61 LAPQRAAPQOKRSSPSEGLCPGGHHSSEDRDICSCKYGQDYSTHWNDLFLCRLCTCD 120
Db 61 LAPQRAAPQOKRSSPSEGLCPGGHHSSEDRDICSCKYGQDYSTHWNDLFLCRLCTCD 120
QY 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTRNTVOCCEGTFRFEDSPMCRCRCRTGCPRGWVKVGDCTPMSDIECVH 180

QY 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDDPERVDRSSORPAED 240
|||||
Db 181 KESGIIIGVTVAAVVLIVAVFVCKSLMKKVLPLYLKGICSGGGDDPERVDRSSORPAED 240
QY 241 NVLNEIVSIILOPTQVPEQEMEOBPAPPTGVNMLSPGSEHLLLEPAEAERSORRLVPA 300
|||||
Db 241 NVLNEIVSIILOPTQVPEQEMEOBPAPPTGVNMLSPGSEHLLLEPAEAERSORRLVPA 300
QY 301 NEGDPTETLRQCDFDADLVFPDSWEPLMKRLGLMDEIVAKAAEAAGHRDITYTMLIKW 360
|||||
Db 301 NEGDPTETLRQCDFDADLVFPDSWEPLMKRLGLMDEIVAKAAEAAGHRDITYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411
|||||
Db 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411
RESULT 4
US-09-811-088-6
; Sequence 6, Application US/09811088
; Patent NO. US20020160446A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGRAMSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER
; FILE REFERENCE: 07334-324001
; CURRENT APPLICATION NUMBER: US/09/811,088
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/712,726
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 08/820,364
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 09/757,421
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 08/843,652
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: US 08/843,651
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: US 09/354,809
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 08/938,365
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-088-6
Query Match 99.9%; Score 2167; DB 10; Length 411;
Best Local Similarity 99.8%; Pred. No. 8e-187;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 241 NVLNEIVSIILOPTQVPEQEMEOBPAPPTGVNMLSPGSEHLLLEPAEAERSORRLVPA 300
|||||
Db 241 NVLNEIVSIILOPTQVPEQEMEOBPAPPTGVNMLSPGSEHLLLEPAEAERSORRLVPA 300
QY 301 NEGDPTETLRQCDFDADLVFPDSWEPLMKRLGLMDEIVAKAAEAAGHRDITYTMLIKW 360
|||||
Db 301 NEGDPTETLRQCDFDADLVFPDSWEPLMKRLGLMDEIVAKAAEAAGHRDITYTMLIKW 360
QY 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411
|||||
Db 361 VNKTGRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNADSAYS 411
RESULT 5
US-09-992-964-11
; Sequence 11, Application US/09992964
; Patent NO. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2dcr
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 11
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 410
; OTHER INFORMATION: Xaa may be leucine or methionine
US-09-992-964-11
Query Match 99.9%; Score 2167; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 8e-187;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-10-052-798-1
Sequence 1, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilla W.
Ashkenazi, Avi J.
Chuntharapal, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-052-798-1
Query Match 99.9%; Score 2167; DB 14; Length 411;
Best Local Similarity 100.0%; Pred. No. 8e-187;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORGQNAAPASGARRKHGPGPREARPGRLVPTLVVAAVLLVSAESALITQOD 60
DB 1 MEORGQNAAPASGARRKHGPGPREARPGRLVPTLVVAAVLLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSPSEGLCPPGHHISEGRODCISCKYGODYTHMNDLFLCRLTRCD 120
DB 61 LAPQORAPPOOKRSPSEGLCPPGHHISEGRODCISCKYGODYTHMNDLFLCRLTRCD 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGIIIGVYVAAVLLVAVFVCKSLMKKVLPLYLKGISGGGGDPRVRDSSORPGAED 240
DB 181 KESGIIIGVYVAAVLLVAVFVCKSLMKKVLPLYLKGISGGGGDPRVRDSSORPGAED 240
QY 241 NVLNEIYSIIQPTVPPEQEMEVQEPAPPTGVNMLSPSESHLEPPAEARSQRRLLYPA 300
DB 241 NVLNEIYSIIQPTVPPEQEMEVQEPAPPTGVNMLSPSESHLEPPAEARSQRRLLYPA 300
QY 301 NEGDPFTLRCQCFDDFADLVFPDSWEPMLMKRLGLMNEIKYAKAEAGHRDLYTMLIKW 360
DB 301 NEGDPFTLRCQCFDDFADLVFPDSWEPMLMKRLGLMNEIKYAKAEAGHRDLYTMLIKW 360

QY 361 VNKTRGRASVHTLLDALETTGERLAKOKIEDHLLSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRASVHTLLDALETTGERLAKOKIEDHLLSGKFMYLEGNADSAXS 411
RESULT 7
US-10-207-655-194
Sequence 194, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069,401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 194
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-194

Query Match 99.9%; Score 2167; DB 15; Length 411;
Best Local Similarity 99.8%; Pred. No. 8e-187;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MEORGQNAAPASGARRKHGPGPREARPGRLVPTLVVAAVLLVSAESALITQOD 60
DB 1 MEORGQNAAPASGARRKHGPGPREARPGRLVPTLVVAAVLLVSAESALITQOD 60
QY 61 LAPQORAPPOOKRSPSEGLCPPGHHISEGRODCISCKYGODYTHMNDLFLCRLTRCD 120
DB 61 LAPQORAPPOOKRSPSEGLCPPGHHISEGRODCISCKYGODYTHMNDLFLCRLTRCD 120
QY 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVQCCEGTFREDSPEMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
QY 181 KESGIIIGVYVAAVLLVAVFVCKSLMKKVLPLYLKGISGGGGDPRVRDSSORPGAED 240
DB 181 KESGIIIGVYVAAVLLVAVFVCKSLMKKVLPLYLKGISGGGGDPRVRDSSORPGAED 240
QY 241 NVLNEIYSIIQPTVPPEQEMEVQEPAPPTGVNMLSPSESHLEPPAEARSQRRLLYPA 300
DB 241 NVLNEIYSIIQPTVPPEQEMEVQEPAPPTGVNMLSPSESHLEPPAEARSQRRLLYPA 300
QY 301 NEGDPFTLRCQCFDDFADLVFPDSWEPMLMKRLGLMNEIKYAKAEAGHRDLYTMLIKW 360
DB 301 NEGDPFTLRCQCFDDFADLVFPDSWEPMLMKRLGLMNEIKYAKAEAGHRDLYTMLIKW 360
QY 361 VNKTRGRASVHTLLDALETTGERLAKOKIEDHLLSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRASVHTLLDALETTGERLAKOKIEDHLLSGKFMYLEGNADSAXS 411
RESULT 8
US-10-314-410-6
Sequence 6, Application US/10314410
Publication No. US20030125540A1
GENERAL INFORMATION:
APPLICANT: Holzman, Douglas A.
APPLICANT: Geating, David P.
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER
FILE REFERENCE: 07334-324001
CURRENT APPLICATION NUMBER: US/10/314,410
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US/09/811,088
PRIOR FILING DATE: 2001-03-16

DR SMART; SM00005; DEATH; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 FT VARIANT 75 75 V -> A.
 FT VARIANT 89 89 E -> K.
 FT VARIANT 196 196 E -> K.
 FT VARIANT 201 201 R -> H.
 SQ SEQUENCE 333 AA; 37468 MW; 98C17F766762F287 CRC64;

Query Match 9.3%; Score 202; DB 6; Length 333;
 Best Local Similarity 22.9%; Pred. No. 2.8e-09;

Matches 88; Conservative 59; Mismatches 134; Indels 104; Gaps 16;

QY VPRTLVVAAVLVLSAESAALITQODLAPQORAPQOKRSSPSGL-----CP 83
 DB LPLVLTIVYVRLSKCVNAQVNDISKGF--ELRKIVTTITFQNLGLHHEGQFCRNPCPP 65
 QY 84 GHH-----ISDGRDCISCKYGGDYSTHMDLFLCLCTRCDSG--EVELSPCTTTRN 134
 DB GERKARDCVTNEDPDVCPQCEGEYTDKGHFSSKCRCLDCGHGLEVEIN-CTPTQN 124
 QY 135 TVCCCEBTEFREEDSPENCRCRCGCPRGMYKVGDCPTWSDIECVHKSGIIGVTVAAV 194
 DB 125 TKCRCKPMPFNCSAVCEHCDPC-TRCKHGIIIE--ECTLTSTMTCKEEDSRSDL----- 174
 QY 195 VLIIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDSSORPPGADNVLEIVSILPTQ 254
 DB 175 -----LWICLLILLLLLPPIYVVIK-----EPCRRKRENGPHESTLTN----- 215
 QY 255 VPGEEMEVOEPAEPTGVNMLSPGESEHLLPEAEERSQRRLLVPANEGDPTETLRQCFD 314
 DB 216 -PE-----TAINLSDVLSKYITTTAGA-----MTLSQVKD 245
 QY 315 DFADLVPPDSMEPLMRKIGLMDNEIKVAKAELAGHRTL---YTMLIKWNKTKGRDASVH 371
 DB 246 -----FVRKNGV--SEAKIDEIKNDVQDTAEQKVOLLRNMYOLHGKKD 290
 QY 372 TLDDALE-----TLGERLAKOKIED 391
 DB 291 TLIGLKTADLCTLAEKIHAVILKD 315

RESULT 9

Q9BDN0 PRELIMINARY: PRT: 331 AA.
 AC Q9BDN0.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE FAS antigen CD95.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RT Immunogenetics 53:315-328(2001).
 RL EMBL; AF344850; AAK37610.1; -
 DR EMBL; AF344850; AAK37610.1; -
 DR HSSP; P25445; IDPF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death.1.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 9.1%; Score 197; DB 6; Length 331;
 Best Local Similarity 22.9%; Pred. No. 7.5e-09;

Matches 88; Conservative 56; Mismatches 135; Indels 106; Gaps 16;

QY 34 VPRTLVVAAVLVLSAESAALITQODLAPQORAPQOKRSSPSGL-----CP 83
 DB LPLVLTIVYVRLSKCVNAQVNDISKGF--ELRKIVTTITFQNLGLHHEGQFCRNPCPP 65
 QY 84 GHH-----ISDGRDCISCKYGGDYSTHMDLFLCLCTRCDSG--EVELSPCTTTRN 134
 DB GERKARDCVTNEDPDVCPQCEGEYTDKGHFSSKCRCLDCGHGLEVEIN-CTPTQN 124
 QY 135 TVCCCEBTEFREEDSPENCRCRCGCPRGMYKVGDCPTWSDIECVHKSGIIGVTVAAV 194
 DB 125 TKCRCKPMPFNCSAVCEHCDPC-TRCKHGIIIE--ECTLTSTMTCKEEDSRSDLPWLCLLL 181
 QY 195 VLIIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDSSORPPGADNVLEIVSILPTQ 254
 DB 182 LLIPPI-----YVVYIKKAC-----RKHKRENGPHESTLTN----- 213
 QY 255 VPGEEMEVOEPAEPTGVNMLSPGESEHLLPEAEERSQRRLLVPANEGDPTETLRQCFD 314
 DB 214 -PE-----TAINLSDVLSKYITTTAGA-----MTLSQVKD 243
 QY 315 DFADLVPPDSMEPLMRKIGLMDNEIKVAKAELAGHRTL---YTMLIKWNKTKGRDASVH 371
 DB 244 -----FVRKNGV--SEAKIDEIKNDVQDTAEQKVOLLRNMYOLHGKKD 288
 QY 372 TLDDALE-----TLGERLAKOKIED 391
 DB 289 TLIGLKTADLCTLAEKIHAVILKD 313

RESULT 10

Q9TSN4 PRELIMINARY: PRT: 331 AA.
 AC Q9TSN4.
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Death receptor Fas (Apo-1/CD95).
 GN FAS.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20237686; PubMed=10773350;
 RA Murayama Y., Terao K., Inoue-Murayama M.;
 RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
 RT Hum. Immunol. 61:474-485(2000).
 RL EMBL; AB031420; BAA83551.1; -
 DR EMBL; AB031420; BAA83551.1; -
 DR HSSP; P25445; IDPF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death.1.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor.

Query Match 9.0%; Score 196; DB 6; Length 331;
 Best Local Similarity 22.9%; Pred. No. 9.2e-09;
 Matches 88; Conservative 56; Mismatches 135; Indels 106; Gaps 16;

```

0Y 34 VPRTVLVAAVALLVVSAAALITOODLAPQOARAPQOKRSSPSEGL-----CP 83
Db 8 LPLVLTSVYRLSLKSCVMAQVDTISSKG--ELRKVYTTETQNLBGLHHGQCFRNP 65
0Y 84 GHH-----ISEDGDCISCKYGODYSTHWMNDLFCRLCTRCDSG--EVELSPCTYTRN 134
Db 66 GERKARDCTVNEDEPDCVPQCGEKETXDKGHFSSKRCRLDEGHGLEVEIN-CTR 124
0Y 135 TVCOEEBGFREDEBSPMCRCRKRTGCPKRMVAVGDCTPMSDIECVHKEGIIIGTVAAV 194
Db 125 TKCRCKPNEFCNSAVCEHDDPC-TCSEHIIIE-ECTLTSMCKEEDSRSDLPWLC 181
0Y 195 VLIYVAVFCKSLMKKVLPLYLKIGTSGGGGDEPRYDRSSQRBGAENNYEISILQ 254
Db 182 LLIPPI-----VYVVIKAC-----RKHKRNQGPHESTLTN----- 213
0Y 255 VPDEMEVOEPAEPTGVNMLSPGESEHLELPAEERSORRRLVLANEGDPTETLRQ 314
Db 214 -PE-----TAINLSDVDLSKTYITTTAGA-----MTLSQVAD 243
0Y 315 DFADLVPEDSWEPLMRKTLGLMDNETIKVAKAEAGHRDTL---YTMILKVNKTRDASV 371
Db 244 -----FVRKNGV--SEAKIDEIKNDNVDTAEQKVQLLRNMYQLHGKKDAD 288
0Y 372 TLLOALE-----TLGERLAKOKIED 391
Db 289 TLIRKGLTADICTLAEKTHAVILKD 313

```

RESULT 11	
Q9BDN4	
ID Q9BDN4	PRELIMINARY;
NC Q9BDN4	PRT; 331 AA

DT	01-JUN-2001	(TREMBLrel. 17, created)
DT	01-JUN-2001	(TREMBLrel. 17, last sequence update)
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)
DE	FAS antigen CD95.	
OS	Cercopithecus torquatus alys (Red-crowned mangabey) (Sooty mangabey).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;	
OC	Cercopitheciinae; Cercopithecus.	
OX	NCBI_TaxID:9531;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE-21383618; PubMed-11491535;	
RA	Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,	
RA	Weiss W.R., Ansari A.A.;	
RT	"Cloning, sequencing, and homology analysis of nonhuman primate	
RT	Fas/FasL ligand and co-stimulatory molecules.";	
RL	Immunogenetics 53:315-328(2001).	
DR	EMBL; AF344843; AAK37602.1; -.	
DR	HSSP; P23445; 1DDE.	
DR	InterPro: IPR000488; Death.	
DR	InterPro: IPR001368; TNFR_c6.	
DR	Pfam: PF000531; death. 1.	
DR	Pfam: PF000020; TNFR_c6; 2.	
DR	SMART; SM00005; DEATH; 1.	
DR	SMART; SM00208; TNFR; 2.	
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 2.	
FT	VARIANT	44 44 I -> V.
FT	VARIANT	47 47 R -> O.
FT	VARIANT	55 55 R -> D.
FT	VARIANT	60 60 R -> H.
FT	VARIANT	61 61 N -> S.
FT	VARIANT	77 77 E -> G.
FT	VARIANT	95 95 G -> A.
FT	VARIANT	282 282 E -> G.
FT	VARIANT	298 298 G -> D.
FT	VARIANT	300 300 C -> *.
SO	SEQUENCE	331 AA; 37277 MW; 1D843C4DE1D343F4 CRC64;

	Best Local similarity	22.9%	Pred. No.	1.2e-08:	
QY	Matches	88;	Conservative	56;	Mismatches 136; Indels 105; Gaps 16
Db	34	VKTLVLVVAAYLLIVSAESALITQODLAPQOARAPDQKRSSPSEGL-----CP	83		
	:	: :	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
Db	8	LPLVTLSVRLLSKCVNAQVDINSKGELFKRIVTTIETRN--LEGLIHGEGFCRNPCP	65		
QY	84	GHH-----ISDGDCISCCKGYDYSTHWNMLFLCLRTRODSG---EVELSPCTTNN	134		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
Db	66	GERRAKDTVNEDDDCVCPOGGKYTPDKGHFSSKCRRCRLDEBHGHEVEIN-CITRON	124		
QY	135	TVCQCEEGNFRREDSPEMCRKCRTPCGPMGVGVGCOTPSMDIECHNKESGIIIGTVAAV	194		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
Db	125	TKCRKKPPFFCSAVCEHDPC-TYCKKHGLE--ECCTLTSNKCCEBDRSPL-----	174		
QY	195	VLIIVAFVKCSILMKKVLPY--LKSGICSGGGDPERVDRSSQPAEDVNLIVSILOP	252		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
Db	175	-----LMICLLLLLPIVIYYIKAC-----RKHKREMGSHESTLN-----	213		
QY	253	TQVPQEOMEVOEPAPFTGVNMISPGESEHLLEPAEAERSQRRLLVANEGDPTETLRQC	312		
	:	:	:	:	:
	:	:	:	:	:
Db	214	--PE-----TAINTSDVDLSKITTIAG-----MTLSQV	241		
QY	313	FDDFEADVLVPDSWEPLMRKLGMONEIVYAKAEAGAHRDL---YTMLIKWYNKTGRDAS	369		
	:	:	:	:	:
	:	:	:	:	:
	:	:	:	:	:
Db	242	RD-----FVRKNQV--SEAKIDEIKNDNVODTAEOKVOLLRNYQLHEKKDA	286		
QY	370	VHTLDALETLLGERLAKQIEDHLL	394		
Db	287	CDTLTKGTAGCTLAERIRHAVIL	311		

RESULT 12	
09GL40	
ID 09GH40	PRELIMINARY;
10 000740	PRT; 334 AA

```

DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Fas antigen.
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxId=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shui B., Chi L., Zhang Y.R.;
RT      "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
RL      Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RR      EMBL: AY007572; AAC16762.1; -.
DR      HSSP; P25445; IDDP.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR001368; TNFR_c6.
DR      Pfam; PF00531; death_1.
DR      Pfam; PF00020; TNFR_c6; 2.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00208; TNFR; 2.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS00652; TNFR_NGFR_1; 2.
DR      PROSITE; PS00509; TNFR_NGFR_2; 2.
SQ      SEQUENCE 334 AA; 37351 MW; 2DC5B161C3191C6 CRC64;

```

Query Match	9.0%;	Score 194.5;	DB 6;	Length 334;
Best Local Similarity	23.6%;	Pred. No. 1.3e-08;		
Matches	03	Conservation	50	117

[illegible]


```

Db      66 GERKARCDTVNDEBDCVPCOGEKEYTDKGFHSSKCRRCRLCDEGHGLEVEIN-CTRTON 124
OY      135 TWCOCEEGTFRDEDSPEMCKRCRTGCPRGVAVGDTCPWSDIECVHKESGIIIGTVAAV 194
Db      125 TRCKRKPFFCNSAVCEHCDCP-TRCKHGLE-ECOTLTSNTCKEEDSRDL----- 174
OY      195 VLIIVAFVCKSLMKRVLP-----YLKIGCSGGGDPFERVDRSSORFGAEDVLEIYSI 249
Db      175 -----LWICLILLILLILLIPPIYVVIKKPC-----RKHKRKNQPHSTTLN----- 216
OY      250 LQPTQVPEDEMVEQPAEPTGVNMLSPGESEHLLPEAEKRSORRRLLVPANEGDPTETL 309
Db      217 -----PE-----TAINLSDVDLSKYITITAGA-----MTL 241
OY      310 ROCFDDPADLVFPDSMEPLMKRLGLMDNEIKYAKAEAGHRDYL---YTMILKMYNKTGR 366
Db      242 SQ-VADFG-----RKNGV--SEAKIDEIKNDVQDTAEQKYOVLKNNIOPHCK 286
OY      367 DASVHTLLDALE-----TLGERLAKQKIED 391
Db      287 KDCACTLIKGLTADLCTLAERKHAIVILKD 316

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RESULT 13

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O95ND3 PRELIMINARY: PRT: 446 AA.
ID 095ND3
AC 095ND3
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Tumor necrosis factor type I.
GN TNFR_I.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "Molecular cloning of feline tumor necrosis factor receptor type I
RT (TNFR I) and expression of TNFR I and TNFR II in various disease in
RT cats.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB051103; BAB5455.1; -.
DR InterPro: IPR000345; Cyrc_heme_bind.
DR InterPro: IPR000488; Death.
DR InterPro: IPR006209; Egf_Like.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_C6; 4.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
SO SEQUENCE 446 AA, 49563 MW, 217BD31D8A74AA CRC64;

```

Query Match 8.8%; Score 191.5; DB 6; Length 446;
 Best Local Similarity 23.0%; Pred. No. 3.4e-08;
 Matches 105; Conservative 55; Mismatches 164; Indels 133; Gaps 23;

```

OY      30 PELRVPKTVLVVAAVLLVSAESALITQDLAPQORAAPOQRSSPSGCLPPGHHSIE 89
Db      7 PELLQP-LVLLA-----LLVEIYPLRVY--GLVPHLR--DREKRAIP-----CPQGYIHP 52
OY      90 DGR-----DCISCKYGQDYSTHNNDLFLCLRCTRC--DSGE 123
Db      53 QDNSTICCTCKHGTLYLNDACAPGLDTCRECENG-TTFASENYLRQCLSCSKCKREKMY 111
OY      124 VELSPCTTNTVCOCEEGTFR--EDSPEMCKRCRTGCPRGVAVG-----DCTPWS 174

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Db      112 VEISPTCYRVDTVCGCRKNQRYRWSETHFOCLNCSL-CLNGTVOISCKETONTVCTCHA 170
OY      175 D-----IECVHRESG-----IIGVTV-----AAVLIYAVP----- 201
Db      171 GFFLLRQNECVCVNCCKNTECKTKLCVPIVETVKDPDQDPTVLLPLVIFFGICVLSFSG 230
OY      202 -VCK-----SLMKVLLPYLKG-----TCSGGGDERVDRSSORFGAEDVLEIYSI 247
Db      231 LMCRRQRRKSKLFLSYVCGSTPTKEEPOPLATGCFSP1PSPPTSPSTFTPS----- 284
OY      248 SLLOPTQVPEQ-----EMEVOEPAEPTGVNMLSPGESEHLLPEAEKRSORRRLLV 298
Db      285 -----PTFTPSDVAHLRAASVSREMAPPYOGAGPIILSAAPASSPISTPVQKWDSTHTQRP 340
OY      299 PANEDDPTETLQOCDDPADLVFPDSMEPLMKRLGLMDNEI-KVAKAEAGHRDLYTML 357
Db      341 EADPADPA-TLYAVVDG-----VPPSRKKEFVRLGLSEHIERLELQNGRCLEAHYSML 395
OY      358 IKWVNKT-----GRDASVHTLLDALELTGERL 384
Db      396 AAMRRRTPRREATLLELGRVLRDMOLLGCLDEIEEAL 432

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RESULT 14

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O99MM1 PRELIMINARY: PRT: 413 AA.
ID 099MM1
AC 099MM1
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE WSL-1-like protein.
GN TNRSF25 OR TNRSF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-129/Sv.
RX MEDLINE-21158384; PubMed-11261933;
RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Ap03, TRAMP, LARD, TR3, TNRSF12)
RT gene.";
RL Immunogenetics 53:59-63(2001).
DR EMBL: AF329569; AAK11256.1; -.
DR HSSP: Q92956; JMA.
DR MGD: MGI:1934667; Tnfslf25.
DR InterPro: IPR000488; Death.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_C6; 3.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
SO SEQUENCE 413 AA, 44453 MW, 69F21B5D0DABABF CRC64;

```

Query Match 8.8%; Score 190; DB 11; Length 413;
 Best Local Similarity 23.6%; Pred. No. 4.1e-08;
 Matches 102; Conservative 47; Mismatches 172; Indels 112; Gaps 24;

```

OY      24 EARGARPGRLVPKTVLVVAAVLLV---SASALITQDLAPQORAAPOQRSSP--SE 78
Db      2 EARLRGCVVEPLFLPILLILLILLIGGGGGSGKRDCASE-----SQRRYGPFCRR 56
OY      79 GLCPRGHHSIE-----DGRDCISCKYGQDYSTHNNDL-LFLCLRCTRCDSG--EVELSPC 129
Db      57 G-CPKGHYWKAPCAEBCGNSLTCLPCP-SDTFLTRDWHFKTDCTRQGVQDDEALQYTLENC 114

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OY      130  TTTNRTVQCEGGTFR-----BDSPEMKRCR-----157
           : : : : :
Db      115  SAKSTHCCGCGSMWCVDSTVPCGSSPFCVPCGATTFVHNEPTFRPLCPGTINGNDC 174
           115  SAKSTHCCGCGSMWCVDSTVPCGSSPFCVPCGATTFVHNEPTFRPLCPGTINGNDC 174
OY      158  TGCPRGMKV--GDCTP--MSDIECVHKEGIIIGTVAAVVLIVAFVCKSLMKKYL 212
           111  TGCPRGMKV--GDCTP--MSDIECVHKEGIIIGTVAAVVLIVAFVCKSLMKKYL 212
Db      175  TSCPGRGFSVCPKATAVCGMKOMWVQ---VLLGV---AFIFAILLCARQOPCK 226
           175  TSCPGRGFSVCPKATAVCGMKOMWVQ---VLLGV---AFIFAILLCARQOPCK 226
OY      213  PYLKICGGG--GDPERVDRSSQ-----RPAEDVNLNEIVSLTOPVQ--RQEME 261
           : : : : :
Db      227  AVVTDATGTERLASQTAHLASDSAHITLLAPRSTGKICTVQLVGNWTFGELQTOE 286
           227  AVVTDATGTERLASQTAHLASDSAHITLLAPRSTGKICTVQLVGNWTFGELQTOE 286
OY      262  V-----QEPAPGVNMLSGEGSEHLLLEPRAAEKSQRRRLVPRANEGDPTETLR- 310
           262  V-----QEPAPGVNMLSGEGSEHLLLEPRAAEKSQRRRLVPRANEGDPTETLR- 310
Db      287  VVCGASQPMDDLPRNLTJSTPLASP-----LSPAP-----PA--GSPAAYLQ 327
           287  VVCGASQPMDDLPRNLTJSTPLASP-----LSPAP-----PA--GSPAAYLQ 327
OY      311  --QCEDDPADLVPPFSWEPLMKRLKGLINDINEIVAKAEAGHNDLTLYMLIKVWNTKGRDA 368
           311  --QCEDDPADLVPPFSWEPLMKRLKGLINDINEIVAKAEAGHNDLTLYMLIKVWNTKGRDA 368
Db      328  GPQLT-DVMDADVAPRRMKFEVRLTGLREAEIEAVEICRFRRDOQYEMLKRW--RQOQPA 384
           328  GPQLT-DVMDADVAPRRMKFEVRLTGLREAEIEAVEICRFRRDOQYEMLKRW--RQOQPA 384
OY      369  SVNHTLLDALETIG 381
           369  SVNHTLLDALETIG 381
Db      385  GIGATYAADERKKG 397
           385  GIGATYAADERKKG 397

```

SEQUENCE	15	RESULT
09GK28	PRELIMINARY;	PRT; 310 AA.
AC 09GK28;		
DT 01-MAR-2001 (TrEMBLrel. 16, Created)		
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)		
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)		
DE Fas antigen Apo-1/CD95.		
GN FAS.		
OS Macaca acroideus (Stump-tailed macaque).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi		
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC Cercopithecinae; Macaca.		
OX NCBI_TaxID=9540;		
RN [1]		
SEQUENCE FROM N.A.		
RA Chl L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;		
RT "Cloning of fas gene in stump-tailed monkey.";		
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.		
RL EMBL: AF32357; AAG49394.1; -		
DR HSSP; P25445; 1DDE.		
DR InterPro; IPR000488; Death.		
DR InterPro; IPR001368; TNFR_C6.		
DR Pfam; PR00531; death_1.		
DR Pfam; PF00020; TNFR_C6; 2.		
DR SMART; SM00005; DEATH_1.		
DR SMART; SM00208; TNFR; 2.		
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.		
DR PROSITE; PSS0050; TNFR_NGFR_2; 2.		
SEQUENCE 310 AA: 34806 MW; C5C799F1E804A419 CRC64;		

Query Match	8.7%	Score 188.5;	DB 6;	Length 310;
Best Local Similarity	22.9%	Pred. No. 3.8e-08;		
Matches	88;	Conservative	50;	Mismatches 120;
			Indels	127;
			Gaps	17;

```

0Y      34 PKRLTVLVAAVALLVSMASALITQODLAPQORAAPOQRKRSSEEL-----CPR 83
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      8 LPLVLTSTVRLRLSKCVMAQVTDISSKG--ELRKIVTITITETONLELHHGDFCRNCP 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      84 GHH-----ISEDGRDCISCKYGQDYSTHWNLLLECLRTRODSG---EVELSPCTTTRN 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      66 GERARDCVTNDEDPDVCVPOEGKRYTQKHGHSKCRRLCDEGHGLEVEIN-CTRON 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y      135 TVVCCSEGTFRDEDSPEMKRCRTGCPRMVAVVGGDTPGSDIECVHKEGSIITGVAAV 194
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      125 TKCRCKPMPFCNSAVCEHDDPC-TICKKHIIIE-ECITLTSNNK--KEEYVI----- 171

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OY      195  VLIYAVVCSSLLMKKUYFLPKLGICGGGGDEDERADRSSRGADNYIVLSLPTQ 254
          ||
          ||
Db      172  -----KK-----PCKHKREKQGNHSTLTN-----192
OY      255  VPDEQMEVQRPAPETGVNMLSPGESEHLLPAPAEERSORRLLYPANEGDPTETLRQCFD 314
          ||
          ||
Db      193  -PE-----TAINLSDVDLSKYITTAGA-----MTLSQVKD 222
          ||
OY      315  DFADLVYFDSNEPLMKLGLMDNEIKVAAAEAGHROL---YTMILKKNVKKTORDSAVH 371
          ||
          ||
Db      223  -----FVKRNGV--SEAKIDIKNNHNVODTAEOKVOLLRNWYQLHKKKDACD 267
          ||
          ||
OY      372  TLDALD-----TLGERLAKOKIED 391
          ||
          ||
Db      268  TLIKGLKTADLCYLAERIKHNAVILKD 292

```

```
Search completed: August 4, 2003, 15:19:42
Job time : 101 secs
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? PRIOR APPLICATION NUMBER: US 09/712,726
? PRIOR FILING DATE: 2000-11-14
? PRIOR APPLICATION NUMBER: US 08/820,364
? PRIOR FILING DATE: 1997-03-12
? PRIOR APPLICATION NUMBER: US 09/757,421
? PRIOR FILING DATE: 2001-01-10
? PRIOR APPLICATION NUMBER: US 08/843,652
? PRIOR FILING DATE: 1997-04-16
? PRIOR APPLICATION NUMBER: US 08/843,651
? PRIOR FILING DATE: 1997-04-16
? PRIOR APPLICATION NUMBER: US 09/354,809
? PRIOR FILING DATE: 1999-07-16
? PRIOR APPLICATION NUMBER: US 08/938,365
? PRIOR FILING DATE: 1997-09-26
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 6
? LENGTH: 411
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-314-410-6

Query Match          99.9%: Score 2167: DB 15: Length 411:
Best Local Similarity 99.8%: Pred. No. 8e-187:
Matches 410: Conservative 0: Mismatches 1: Indels 0: Gaps 0:

```

Query Match	99.9%	Score 2167	DB 15	Length 411
Best Local Similarity	99.8%	Pred. No. 8e-187		
Matches 410	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY 1	MEORGQAAPASGARKRHGPGREARGARPELRPKTLVLVVAVLLVSAESALITQOD	60		
Db 1	MEORGQAAPASGARKRHGPGREARGARPELRPKTLVLVVAVLLVSAESALITQOD	60		
QY 61	LAPQGRAAPOOKRSSPSBGLCPRHNIISEDRODISCYGGDYSTHNDLLFLCLRTGCD	120		
Db 61	LAPQGRAAPOOKRSSPSBGLCPRHNIISEDRODISCYGGDYSTHNDLLFLCLRTGCD	120		
QY 121	SGEVELSPCTTTRNTVQCCEGTEPREDESPEMCKRCRTGCRGMKVGDCTPMSDIECVH	180		
Db 121	SGEVELSPCTTTRNTVQCCEGTEPREDESPEMCKRCRTGCRGMKVGDCTPMSDIECVH	180		
QY 181	KESGIITGVAAVVLIVAVFVCKSLMKKVLPLYLKGISGGGGGPERHYDRSSORPGAED	240		
Db 181	KESGIITGVAAVVLIVAVFVCKSLMKKVLPLYLKGISGGGGGPERHYDRSSORPGAED	240		
QY 241	NVLNEIYSLIOPVPOEMEVORPAEPTGVNMLSPGSEHLLPFAERERORRLTLPVA	300		
Db 241	NVLNEIYSLIOPVPOEMEVORPAEPTGVNMLSPGSEHLLPFAERERORRLTLPVA	300		
QY 301	NEGDPTETLRQCFDFADLVPFDSEWERMRLRLGLMDNEIKAKAAEAAHBDTLVYMLTKW	360		
Db 301	NEGDPTETLRQCFDFADLVPFDSEWERMRLRLGLMDNEIKAKAAEAAHBDTLVYMLTKW	360		
QY 361	VNKTGRASVHTLLDAETLGERLAKOKIDENHLLSSGFMYLLEGNADSAXS	411		
Db 361	VNKTGRASVHTLLDAETLGERLAKOKIDENHLLSSGFMYLLEGNADSAXS	411		

```

RESULT 9
US-10-067-615-2
:
: Sequence 2, Application US/10067615
: Publication No. US20020115154A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Alimet, Emad S.
: TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
: FILE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 480140.432D1
: CURRENT APPLICATION NUMBER: US/10/067.615
: CURRENT FILING DATE: 2002-02-04
:
: NUMBER OF SEQ ID NOS: 6
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 2
:
: LENGTH: 411
:
: TYPE: PR1
:
: ORGANISM: Homo sapiens
: US-10-067-615-2

```

Query Match	99.78;	Score 2163;	DB 14;	Length 411;
Best Local Similarity	99.58;	Pred. No. 1.8e-186;		
Matches 409;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	MEQKQNAAPASGARKRHGCPREARGARPLAVPKTYLVAAVALLVSAESALITQOD	60
Db	1	MEQKQNAAPASGARKRHGPPEPREARGARPLAVPKTYLVAAVALLVSAESALITQOD	60
QY	61	LAPQORAPAPQOKRSSPSEGLCPPGHHISSEDRDCISCKYGDYSTHWNDDLFFCLRCTPCD	120
Db	61	LAPQORAPAPQOKRSSPSEGLCPPGHHISEDRDCISCKYGDYSTHWNDDLFFCLRCTPCD	120
QY	121	SGEYELSPCTTTTRNTVCCCEBGTREEDSPEMCKRCKRTGCPRGMYKVGDCITPMSDIECVH	180
Db	121	SGEYELSPCTTTTRNTVCCCEBGTREEDSPEMCKRCKRTGCPRGMYKVGDCITPMSDIECVH	180
QY	181	KESGIIIGVWAAVYLIVAVFCSLSLMKATLYPLTKGISGSGGGDPREVDSSORPGAD	240
Db	181	KESGIIIGVWAAVYLIVAVFCSLSLMKATLYPLTKGISGSGGGDPREVDSSORPGAD	240
QY	241	NVLNEIYVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRRLVPA	300
Db	241	NVLNEIYVSILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEAEARSQRRRLVPA	300
QY	301	NEGDPETTLROCFDDFADLVFPDSMEPLMRKIGLMDNEIKVAKAEAGHRDTLYTMLIK	360
Db	301	NEGDPETTLROCFDDFADLVFPDSMEPLMRKIGLMDNEIKVAKAEAGHRDTLYTMLIK	360
QY	361	VNKGGRDASVHTLLDALETTLGEERLAKOKIEHLLSSSGKFMVLEGNADSAXS	411
Db	361	VNKGGRDASVHTLLDALETTLGEERLAKOKIEHLLSSSGKFMVLEGNADSAXS	411

```

: RESULT 10
US-10-076-754-2
: Sequence 2, Application US/10076754
: Publication No. US20020161195A1
: GENERAL INFORMATION:
: APPLICANT: Alnemurl, Enad S.
: TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 480140.432D3
: CURRENT APPLICATION NUMBER: US/10/076,754
: CURRENT FILING DATE: 2002-02-12
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-076-754-2

```

Query Match	Similarity	99.7%	Score	2163	DB	14	Length	411
Best Local	Similarity	99.5%	Pred. No.	1,8e	186			
Matches	409	Conservative	0	Mismatches	2	Indels	0	Gaps
QY	1	MEQRGQNPAPASGARKRHGPGPREARGARPGLRVPKTLVLVAAVALLVSAESALITQOD	60					
DB	1	MEQRGQNPAPASGARKRHGPGPREARGARPGLRVPKTLVLVAAVALLVSAESALITQOD	60					
QY	61	LAPQORAPAPQOKRSSPSEGLCPGPHHISEDGDCISCKYGGDYSTHNMDDLFCILRCTKCD	120					
DB	61	LAPQORAPAPQOKRSSPSEGLCPGPHHISEDGDCISCKYGGDYSTHNMDDLFCILRCTKCD	120					
QY	121	SGEVELSPTTTRNTVCCCEGTPEEDSPCEMKCRKCRTPGCRGMVYKVDCTPMSDIECVH	180					
DB	121	SGEVELSPTTTRNTVCCCEGTPEEDSPCEMKCRKCRTPGCRGMVYKVDCTPMSDIECVH	180					
QY	181	KESGIITGVTAAVLVIAVAVCKSLMKKKLPLTKIGTCSGGGGPREVDSSQPGAGD	240					
DB	181	KESGIITGVTAAVLVIAVAVCKSLMKKKLPLTKIGTCSGGGGPREVDSSQPGAGD	240					

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Qy 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Db 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Qy 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Db 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Qy 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
Db 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 11
US-10-076-773-2
: Sequence 2, Application US/10076773
: Publication No. US20020161196A1
: GENERAL INFORMATION:
: APPLICANT: Alnemuri, Emad S.
: TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
: FILE REFERENCE: 480140.432D2
: CURRENT APPLICATION NUMBER: US/10/076,773
: CURRENT FILING DATE: 2002-02-12
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-076-773-2

Query Match 99.7%; Score 2163; DB 14; Length 411;
Best Local Similarity 99.5%; Pred. No. 1,8e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEORGONAPPAASGARRKRRHGGPREARAGAPRLRVPKTLVLYAAVLLVSAESALITQOD 60
Db 1 MEORGONAPPAASGARRKRRHGGPREARAGAPRLRVPKTLVLYAAVLLVSAESALITQOD 60
Qy 61 LAPQORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTRCD 120
Db 61 LAPQORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTRCD 120
Qy 121 SGEVELSPCTTTRNTVQCCCEGTFRREDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTRNTVQCCCEGTFRREDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVH 180
Qy 181 KESGIIIGVYAAVAVLVAVFVCKSLMKKVLPLYLKIGICSGGGGDPERVDRSSORPGAED 240
Db 181 KESGIIIGVYAAVAVLVAVFVCKSLMKKVLPLYLKIGICSGGGGDPERVDRSSORPGAED 240
Qy 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Db 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Qy 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Db 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Qy 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
Db 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 12
US-09-874-138-2
: Sequence 2, Application US/09874138
: Patent No. US20020072091A1
: GENERAL INFORMATION:
: APPLICANT: Ni, Jian
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Yu, Guo-Liang
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```
APPLICANT: Rosen, Craig A.
: TITLE OF INVENTION: Death Domain Containing Receptor 5
: FILE REFERENCE: 1488.1310006
: CURRENT APPLICATION NUMBER: US/09/874,138
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/565,009
: PRIOR FILING DATE: 2000-05-04
: PRIOR APPLICATION NUMBER: 60/148,939
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/133,238
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/132,498
: PRIOR FILING DATE: 1999-05-04
: PRIOR APPLICATION NUMBER: 09/042,583
: PRIOR FILING DATE: 1998-03-17
: PRIOR APPLICATION NUMBER: 60/054,021
: PRIOR FILING DATE: 1997-07-29
: PRIOR APPLICATION NUMBER: 60/040,846
: PRIOR FILING DATE: 1997-03-17
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-874-138-2

Query Match 99.6%; Score 2160; DB 9; Length 411;
Best Local Similarity 99.5%; Pred. No. 3.4e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEORGONAPPAASGARRKRRHGGPREARAGAPRLRVPKTLVLYAAVLLVSAESALITQOD 60
Db 1 MEORGONAPPAASGARRKRRHGGPREARAGAPRLRVPKTLVLYAAVLLVSAESALITQOD 60
Qy 61 LAPQORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTRCD 120
Db 61 LAPQORAAPQOKRSSPSEGLCPGHNHISEDGRDCISCKYGODYSTHNMNLLFCLRCTRCD 120
Qy 121 SGEVELSPCTTTRNTVQCCCEGTFRREDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVH 180
Db 121 SGEVELSPCTTTRNTVQCCCEGTFRREDSPEMCKRCRTGCPRGWKVGDCTPMSDIECVH 180
Qy 181 KESGIIIGVYAAVAVLVAVFVCKSLMKKVLPLYLKIGICSGGGGDPERVDRSSORPGAED 240
Db 181 KESGIIIGVYAAVAVLVAVFVCKSLMKKVLPLYLKIGICSGGGGDPERVDRSSORPGAED 240
Qy 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Db 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGESEHLLLEPAEERSQRRLLVPA 300
Qy 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Db 301 NEGPTETLRQCFDFADLVFPDSWEPLMRKLGIMDNEIKYAKAEAGHRTLYTMLIKW 360
Qy 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
Db 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 13
US-10-039-785-3
: Sequence 3, Application US/10039785
: Publication No. US20020067646A1
: GENERAL INFORMATION:
: APPLICANT: Salcedo et al.
: TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
: FILE REFERENCE: P550
: CURRENT APPLICATION NUMBER: US/10/039,785
: CURRENT FILING DATE: 2002-05-07
: PRIOR APPLICATION NUMBER: 60/369,860
: PRIOR FILING DATE: 2002-04-05
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PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 3
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-3

Query Match 99.6%; Score 2160; DB 13; Length 411;
Best Local Similarity 99.5%; Pred. No. 3,4e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGONAPASAGARRHGGPREANGARGLVPTLVVAVALLSAESALITQOD 60
DB 1 MEORGONAPASAGARRHGGPREANGARGLVPTLVVAVALLSAESALITQOD 60
QY 61 LAPQORAPPOKRSSEGLCPGHHHISEDGRDCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAPQORAPPOKRSSEGLCPGHHHISEDGRDCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVCOCEEGTFREDSPEMCKRCRTGCPGMVYVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVCOCEEGTFREDSPEMCKRCRTGCPGMVYVGDCTPMSDIECVH 180
QY 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICGGGGDPERVDRSSORGAED 240
DB 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICGGGGDPERVDRSSORGAED 240
QY 241 NVLNEIYSILOPQVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300
DB 241 NVLNEIYSILOPQVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300
QY 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKLGLMDNEIKVAKAEAGHRDLYTMLIKW 360
DB 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKLGLMDNEIKVAKAEAGHRDLYTMLIKW 360
QY 361 VNKTRGDAVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411
DB 361 VNKTRGDAVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411

RESULT 14
US-10-005-842-2
Sequence 2, Application US/10005842
Publication No. US20020098550A1
GENERAL INFORMATION:
APPLICANT: NI, Jian
Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
TITLE OF INVENTION: Death Domain Containing Receptor 5
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville

STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,583
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hoover, Kenley
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PP366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-005-842-2
Query Match 99.6%; Score 2160; DB 13; Length 411;
Best Local Similarity 99.5%; Pred. No. 3,4e-186;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGONAPASAGARRHGGPREANGARGLVPTLVVAVALLSAESALITQOD 60
DB 1 MEORGONAPASAGARRHGGPREANGARGLVPTLVVAVALLSAESALITQOD 60
QY 61 LAPQORAPPOKRSSEGLCPGHHHISEDGRDCISCKYGQDYSTHNDLLFCLRCTCD 120
DB 61 LAPQORAPPOKRSSEGLCPGHHHISEDGRDCISCKYGQDYSTHNDLLFCLRCTCD 120
QY 121 SGEVELSPCTTNTNTVCOCEEGTFREDSPEMCKRCRTGCPGMVYVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTNTNTVCOCEEGTFREDSPEMCKRCRTGCPGMVYVGDCTPMSDIECVH 180
QY 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICGGGGDPERVDRSSORGAED 240
DB 181 KESGIIIGTVAAVVLIVAFVCKSLMKKVLPLYLKGICGGGGDPERVDRSSORGAED 240
QY 241 NVLNEIYSILOPQVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300
DB 241 NVLNEIYSILOPQVPEQEMEVOEPAEPTGVNMLSPGSESHLLPEAEERSQRRLLVPA 300
QY 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKLGLMDNEIKVAKAEAGHRDLYTMLIKW 360
DB 301 NEGDPTETLRQCFDDADLVPPDSWEPMLMKLGLMDNEIKVAKAEAGHRDLYTMLIKW 360
QY 361 VNKTRGDAVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411
DB 361 VNKTRGDAVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411

RESULT 15
US-08-916-625B-2
Sequence 2, Application US/08916625B
Publication No. US20010010924A1
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
YOUNG, PETER R.

Db 122 NGSECLPDQACEVCKK-SRCKEDETETSCSTASINIVCKRNSGSGSTSTFTIYIMPLI 180
 QY 199 AVEVCKSIL--WKVLPYKIGICSGG-----GDPERVDRSSQRPAGEEDNVLEIVS 248
 Db 181 VLLACVLCIYVWTSKONKTAVTSPREMKICGDEEVEEKN---DANSRIDDS 237
 QY 249 ILQPTQVPEDEMEVOEPAEPTGVNMLSPGESEHLLPEAERSQRRLLVPAVEDPIET 308
 Db 238 QLAG-----FILEQVVESSSRRLVPLSGE-----ES 264
 QY 309 LRQCFDDFADLVPPDSWEPRLKRLGLMDEIKVAAEAAGHDITLYMLIKVNTGGR 368
 Db 265 LKRTDFEE-IVHYHNRFFRLIGLSDNAIK--SAESLFFEDRVYELKIMKEGELKA 321
 QY 369 SVHTLLDALFTIGERLAKOTIEDHLLSGKFWYLE 403
 Db 322 DFNSLIDALYILDORLSAENIANKAINNSCFKYE 356

RESULT 6

Q9BY82 PRELIMINARY: PRT: 48 AA.
 AC Q9BY82:
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Death receptor 5 (Fragment).
 GN DR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshida T., Maeda A., Tani N., Sakai T.
 RT "Promoter structure and transcription initiation sites of the human
 death receptor 5 gene."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB054004; BAB39708.1;
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 48 AA: 5008 MW: E90E27D81A5EF30A CRC64;

Query Match 10.7%; Score 233; DB 4; Length 48;
 Best Local Similarity 97.9%; Pred. No. 4.3e-13;
 Matches 47; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEORGONAPASGARRHGPPREARGARGLRVEKTLVLYVAAYLL 48
 Db 1 MEORGONAPASGARRHGPPREARGARGLRVEKTLVLYVAAYLL 48
 RESULT 7
 Q9VD70 PRELIMINARY: PRT: 387 AA.
 ID Q9VD70:
 AC Q9VD70:
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Similar to tumor necrosis factor receptor superfamily, member 12.
 DE TNFRSF25 OR TNFRSF12.
 GN TNFRSF25 OR TNFRSF12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straussberg R.
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC017526; AAH1756.1;
 DR MGD: MGI:193467; Tnf1f25.
 DR InterPro: IPR000488; Lach.

DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death. 1.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00005; DEATH.1.
 DR SMART: SM00208; TNFR. 2.
 DR PROSITE: PSS0017; DEATH_DOMAIN. 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00652; TNFR_NGFR_2; 1.
 DR PROSITE: PS00505; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 387 AA: 41640 MW: F1664466BAD68D3 CRC64;

Query Match 9.5%; Score 206; DB 11; Length 387;
 Best Local Similarity 24.7%; Pred. No. 1.5e-09;
 Matches 101; Conservative 46; Mismatches 176; Indels 86; Gaps 23;

QY 15 RKRHGRPREARARG--LRVKTLYLYVAAYLLV---SASALITQODLAPQORAAAP 69
 Db 7 RERSPPG-----AATGSTARVLPFLPLLLLLLLGGGGGSGSGRCDCASE----- 56
 QY 70 QOKRSP--SEGICPPGHHS-----DGRDCISCKYGQDYSTHWNDL-LFCLRCTCD 120
 Db 57 SQRRTPFCRCRG-CPKGHYKAPCAEPCGSGTCLPCD-SPTFLTRDNHFTDCTRCQVCD 114
 QY 121 SG--EVELSPCTTTRNTYQCEGTEREDSPEMCRKCRGCGRYGVGDCTPWSDIEC 178
 Db 115 EELQVLTLEKCSAKSSTHGCQSG-----WCYDCSRE-PCGKSSPSCVPCGATTP 164
 QY 179 VKRESGIT--IGTVAAVLYLYAVFYCKSLMKKVLPLYKIGICSGG--GDPERVDRSSQ 234
 Db 165 VHEAPYPLFWOVLLGVAFLEGAILLCAVCRMPCKAAVYADTAGETTLSPOTAHLSAS 224
 QY 235 -----RGAEDNVNLEIYSILOPTQVP--EOEMEY-----QEPAPPTGVNLS 275
 Db 225 DSAHTLLAPSSGKICTYQVGVNMTPELSSTQGVYVCGAQQPMQQLNRLGTGLAS 284
 QY 276 PGSEHLLPEAERSQRRLLVPAVEDPIETLR---QCFDDFADLVPPDSWEPRLKRL 332
 Db 285 P-----LSRAP-----PA--GSPAVALQPGPOLY-DVMDAVPARRMKEFVRTL 324
 QY 333 GLMDNEIKVAKAAGHROTLYMLIKVWKKTRGRDASVHTLLDALETGL 381
 Db 325 GLREAEIIEAVEICRPDOQYEMLRKW--RQOQPGALGAIYALERMG 371

RESULT 8

Q9BDP2 PRELIMINARY: PRT: 333 AA.
 ID Q9BDP2:
 AC Q9BDP2:
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE FAS antigen CD95.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules."
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344833; AAK37529.1;
 DR HSSP: P25445; 1DDF.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death. 1.
 DR Pfam: PF00020; TNFR_c6; 2.

```

Db      2  RSAAALRLCPVLLLFPAEVL-----GSAAVKKRAARSDLOKPKDLRRKCPMGEYE 52
Qy      88  SEDGRDCISCRYG(Y)STHNDLFLCRLCTRCDSGEVLSPTTNTANTVQCEEGTFRRE 147
Db      53  ANDSIQCLPSK-KKETTEYPNDPPKCLGCRCTREDQVEVSFCIPTFRNTQACAKNGTCLP 111
Qy      148  DSP-EMCRKCRTPCGPMGVVGDCTPMSDEC-----YHKESG---IIISVTAVALIIV 198
Db      112  DHCCEMCKQCKQTEC?GGQVRLAPCTQHSDLCCGPPLEISSSTLWITITFTVLAVALIG 171
Qy      199  AAFVCKSLMKVLPYLKIGCS-----GGGGDPER-----VDRSSQPAEDNVLNEIV 247
Db      172  LVLV-----FMKR-----CSSRHGAGDDGELSMKPSAVNRLQRLQIONRCNE-- 217
Qy      248  SLQPTQVPEQEMEV-EPAPPTGVNMLSPGSEHLLLEPAEERSQRRLLVPANEGDPT 307
Db      218  GIVYQNOQOQELLFTAGSEVPNGEVN-EGTERRTDP---KVETQRLVPLIGENPIA 271
Qy      308  TLROCFDDPADLVPEPDSWPEPLMKRLGLMDNEIKVAKAAGHDTLYTMLIKVNTGTGRD 367
Db      472  LHRSENFVDVVPPEWKRFRGRLDLOENDLTLAQHDVRVSCPEPYQMLNTWLNQGSK 331
Qy      368  ASVHTLLDALLETGLERLAKOKIEDHLLSSGKPMY 401
Db      332  ASVNTLLETLPRIGLSGVADIIASELISKGYOY 365

```

RESULT 4

```

Q9DFV0  ID  Q9DFV0  PRELIMINARY:  PRT:  438 AA.
AC  Q9DFV0:
DT  01-MAR-2001 (Tremblrel. 16, Created)
DT  01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT  01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE  Ovarian TNF receptor.
OS  TNFRSF4.
CN  Brachydanio rerio (zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Bobe J., Goetz F.W.;
RT  "Molecular cloning and expression of a TNF receptor and two TNF
RT  ligands in the fish ovary."
RL  Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).
DR  EMBL; AF250042; AAC24365.1;
DR  HSSP; Q92956; IJMA.
DR  ZFIN; ZDB-GENE-010802-1; tnfrsf4.
DR  InterPro: IPR000345; CytC_heme_bind.
DR  InterPro: IPR000488; Death.
DR  InterPro: IPR001368; TNFR_c6.
DR  Pfam; PF00531; death.1.
DR  SMART; SM00208; TNFR_c6; 3.
DR  PROSITE; PS00190; CYTOCHROME_C_1.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
KW  Receptor.
SQ  SEQUENCE 438 AA; 49103 MW; B7E512BE6E80B04 CRC64;

```

Query Match 13.2%; Score 285.5; DB 13; Length 438;
 Best Local Similarity 25.7%; Pred. No. 2,1e-16;
 Matches 113; Conservative 63; Mismatches 176; Indels 87; Gaps 19;

```

Qy      38  LVVVAALVLLVSAESALITQODLAPQARAPO---QKRSSPEGL---CPGHHISE 89
Db      11  MALVTFSLVGHGAELGVAD--HQNRTAROMTCLLENHEYPHNGFCCKNCAGTYVKE 68
Qy      90  D-----GRDCISCRYGQDYSTHNDLFLCRLCTRCDSGEVLSCTTTRNTVQCEEG 142

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Db      69  KCTSGHWNGK-CSPECNG-TYAEHPTEGMEQCLQSCQCHRDQTVAAECTSTNTKCDKFG 126
Qy      143  TFEEDSP-EMCRKCRTPCGPMGVVGDCTPMSDECYHKES-----GI 185
Db      127  TFCPLPDEPCEVCKKC-TCKRADEEVSQCTYTSNCKRRRSYPTGPTKPSASNSTGT 185
Qy      186  IIGVTAVALIIVAVFCKSLMKVLPYLKIGCSGGGDDPERV-----DRSSQRCGA 238
Db      186  IF-VIVSILLVLICTVGAIFLKRGRQO---SENGNIEEVKVPDECPREEDEN 241
Qy      239  EDVNLNIVSLQPTQVPEQEMEVQEP-----EPYGV-----NMLSPGSEHLL 283
Db      242  SRNAGLEKEEHEHRESNPLOETQETGSKSIPVEDBRGLGDSLPHKNQLFPRPSIAL 301
Qy      284  -----EPAEERSQRRLLVPANEG--DP-----TETLRQCFDDPADLVPE 322
Db      302  PQNHMGFTVPAPRPDRPPEIRLNHGHGDDPRKLLPLGEEESLSKFDLP-DSLIV 360
Qy      323  DSWPEPLMKRLGLMDNEIKVAKAAGHDTLYTMLIKVNTGTGRDASVHTLLDALLETGL 382
Db      361  RYHNKFRSISGVSDNSIKLAETQOP--MDKVYLLRVMMKREGIRANINTLLQALLDLDQ 418
Qy      383  RLAKOKIEDHLLSSGKPMY 401
Db      419  RYSAEHIAKAVERGYYKY 437

```

RESULT 5

```

Q9DF34  ID  Q9DF34  PRELIMINARY:  PRT:  357 AA.
AC  Q9DF34:
DT  01-MAR-2001 (Tremblrel. 16, Created)
DT  01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT  01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE  Death receptor.
OS  Brachydanio rerio (zebrafish) (Danio rerio).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
OX  NCBI_TaxID=7955;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT  "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
RT  receptor in transgenic zebrafish."
RL  Nat. Cell Biol. 0:0-0(2000).
DR  EMBL; AF302789; AAG21396.1;
DR  HSSP; Q92956; IJMA.
DR  InterPro: IPR000488; Death.
DR  InterPro: IPR001368; TNFR_c6.
DR  Pfam; PF00531; death.1.
DR  SMART; SM00208; TNFR_c6; 3.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; 3.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
KW  Receptor.
SQ  SEQUENCE 357 AA; 40662 MW; 1652B4840D9EBDA CRC64;

```

Query Match 13.0%; Score 282; DB 13; Length 357;
 Best Local Similarity 25.8%; Pred. No. 3,3e-16;
 Matches 102; Conservative 59; Mismatches 160; Indels 74; Gaps 15;

```

Qy      41  VVAVALVLSAESALITQODLAPQARAPO--KRSSPEGL-----CPGHHI 87
Db      4  ITLVILLVLLVNNARSHGDLVAHRSVKNRLSDVSCREGLERPHENICCLNCPACTIV 63
Qy      88  -----SENGRCISCRYGQDYSTHNDLFLCRLCTRCDSGEVLSCTTTRNTVQCE 140
Db      64  KKCAAAAEKG-VCAPER-DYTEHDHGLKICSDCKRIDDETIKCTSTQWTRCKR 121
Qy      141  EGTFRSDSP-EMCRKCRTPCGPMGVVGDCTPMSDECYHKES-GIIGVTAVALIIV 198

```


Best Local Similarity 33.3%, Pred. No. 3, Mismatches 15,
Matches 130; Conservative 51; Mismatches 15,

Indels 50; Gaps 11;

QY KTVLVAAVLLVSAESALITQDLAPQRAAPQKRSSPSEGI
Db 2 RSALRCPVLLLLAKVHL-----GSAAVKRAVSP
QY 88 SEDGRDICTCKYGGDYTHMNDLLFCLRCTRCU
Db 53 ANDSSRCLPCK-KDEYTEYENDFPKCLGCRFCRE
QY 148 DSP-EMCKRCRTGCPRGVAVKGDCTPMSDIEC
Db 112 DHPCEMCKCOTRCPCGOVRIACCTQOSDLRGC
QY 199 AVEYCKSLMKVLPYLKIGCSGGGDPERYDT
Db 172 LVLLCCCC-----CRYSAGSGVLSRK
QY 254 QVPEQEMVEQPAE-PTGVNMLSPGSEHL
Db 222 QQQQQOQLLTTEQSEVPGVEV-----EVEEV
QY 312 CFDFADLPVDFDSWEPLMRKLGMDNEIKV
Db 276 SEFTFVDLPVPPQMRFRGRALGLKRNINLYQ
QY 372 TLDALETTLGERLAKOKIEDHLLSSGKEM
Db 336 TLETLTSLQISLSGVADIASLLINGYFOY
365

RESULT 2
QY 09IAR7 PRELIMINARY; PRT; 168 AA.
AC 09IAR7 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last seq.
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TVBS1.
GN TVB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; C.
OC Archosauria; Aves; Neognathae; Anatata; Vertebrata; Euteleostomi;
OC Gallus.
OC NCBI_TaxID=7031;
RN [1]
RX SEQUENCE FROM N.A. PubMed.
RA Adkins H.B., Brojatsch J., Young J.A.T.;
MEDLINE=20193796; PubMed.
RT Subgroups B/D/E Avian Leukosis Viruses Reveals a TNFR-related Receptor for
RT Required Specifically for Cytositis Viruses Reveals Cysteine Residues
RL J. Virol. 74:3572-3578(2000) [group E Virus Entry].
DR HSSP: O14763; IDOG.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR000488; Death.
DR Pfam: PF000531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 1.
DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50050; TNFR_NGFR; 2.
SQ SEQUENCE 368 AA; 4153 MW; 0553CE531DEB47C6 CRC64;

Query Match 21.8%; Score 473; DB 13; Length 368;
Best Local Similarity 33.8%; Pred. No. 7, 7e-33;
Matches 133; Conservative 48; Mismatches 155; Indels 58; Gaps 13;

36 KTVLVAAVLLVSAESALITQDLAPQRAAPQKRSSPSE-----GLCPGHHH 87

Db 2 RSALRCPVLLLLFAEVOL-----GSAAVKRAVSP
QY 88 SEDGRDICTCKYGGDYTHMNDLLFCLRCTRCDSGEVLELSCCTTRNTVCCCEGTFREE 147
Db 53 ANDSIQCLPCK-KDEYTEYENDFPKCLGCRFCREDOVEVSPICPTFRNOCACKNGTCLP 111
QY 148 DSP-EMCKRCRTGCPRGVAVKGDCTPMSDIEC-----VHKEGSG---IIIGTVAAVLI 198
Db 112 DHPCEMCKCOTRCPCGOVRIACCTQOSDLRGCPLLEISSSSTLMIITTVLLAVLG 171
QY 199 AVEYCKSLMKVLPYLKIGCS-----GGGDPER-----VDRSSORPGAEDVNLIV 247
Db 172 LVLY-----FMKR-----CSSHHGAGDGGELSMKSAVAVNRLRLGLIDNRNCE-- 217
QY 248 SILOPTQVPEQEMVEQPAEPTGVNMLSPGSEHLLEPAEERSORRLVLPANEGDTE 307
Db 218 QIYONQOQQLLTFTAQSEVPGVEM--EGTERTPP-----KVETORKLVLEENIA 271
QY 308 TLRCDFADLPVDFDSWEPLMRKLGMDNEIKVAKAAGHRDLYTMLIKWVKTGRD 367
Db 272 LHRSEFTFVDYVFPPEKRRGRALDLDQENDLYLAQDRVSCPEPTOMLTWLNQOSK 331
QY 368 ASVHTLDALETTLGERLAKOKIEDHLLSSGKEM 401
Db 332 ASVHTLLETLPRIQLSGVADIASLLISKGYFOY 365

RESULT 3
QY 09PW79 PRELIMINARY; PRT; 368 AA.
AC 09PW79 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE TVBS3.
GN TVB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A. PubMed-8945512.
RA Brojatsch J., Naughton J., Kolls M.W., Ziegler K., Young J.A.;
RT "CARL, a TNFR-related protein, is a cellular receptor for cytopathic
RT avian leukosis-sarcoma viruses and mediates apoptosis."
RL Cell 87:845-855(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Brojatsch J., Naughton J., Young J.A.T.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF161712; AAD47256.1;
DR HSSP: O14763; IDOG.
DR InterPro: IPR001450; 4Fe4S_ferredoxin.
DR InterPro: IPR000488; Death.
DR Pfam: PF000531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 1.
DR PROSITE: PS00198; 4Fe4S_FERREDOXIN; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS50052; TNFR_NGFR; 1.
DR PROSITE: PS50050; TNFR_NGFR; 2.
SQ SEQUENCE 368 AA; 4151 MW; F558C225AB3750BB CRC64;

Query Match 21.3%; Score 463; DB 13; Length 368;
Best Local Similarity 33.5%; Pred. No. 5, 7e-32;
Matches 132; Conservative 48; Mismatches 156; Indels 58; G

36 KTVLVAAVLLVSAESALITQDLAPQRAAPQKRSSPSE-----GLCPGPG 87

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 4, 2003, 15:14:35 ; Search time 98 Seconds

(without alignments)
102,241 Million cell updates/sec

Perfect score: 2169

Sequence: 1 MEORGQNAAPASGARRK...HLSSGKFMYLEGNADSAXS 411

Scoring table: BLOSUM62

Gapop 10.0, Weight 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriophage:
17: sp_archaeal:

Pred. No. is the number of results predicted of the result being printed,
score greater than or equal to the score core distribution,
and is derived by analysis of the total s

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	22.5	368	13	057408 meagris g
2	473	21.8	368	13	057408 meagris g
3	463	21.3	368	13	057408 meagris g
4	285.5	13.2	438	13	057408 meagris g
5	282	13.0	357	13	057408 meagris g
6	233	10.7	48	4	057408 meagris g
7	206	9.5	387	11	057408 meagris g
8	202	9.3	333	6	057408 meagris g
9	197	9.1	331	6	057408 meagris g
10	196	9.0	331	6	057408 meagris g
11	194.5	9.0	331	6	057408 meagris g
12	194.5	9.0	331	6	057408 meagris g
13	191.5	8.8	446	6	057408 meagris g
14	190	8.7	310	6	057408 meagris g
15	188.5	8.4	328	6	057408 meagris g
16	183	8.4	328	6	057408 meagris g

17	183	8.4	331	6	057408 meagris g
18	181.5	8.3	327	13	057408 meagris g
19	179.5	8.3	327	6	057408 meagris g
20	178.5	8.2	312	13	057408 meagris g
21	176	8.1	302	13	057408 meagris g
22	173.5	8.0	320	6	057408 meagris g
23	171	7.9	285	13	057408 meagris g
24	171	7.9	319	6	057408 meagris g
25	165.5	7.6	130	6	057408 meagris g
26	165.5	7.6	348	12	057408 meagris g
27	163.5	7.5	348	12	057408 meagris g
28	163.5	7.5	349	12	057408 meagris g
29	163.5	7.5	349	12	057408 meagris g
30	163.5	7.5	349	12	057408 meagris g
31	163	7.5	263	6	057408 meagris g
32	161.5	7.4	348	12	057408 meagris g
33	161.5	7.4	351	12	057408 meagris g
34	160.5	7.4	349	12	057408 meagris g
35	159	7.3	457	4	057408 meagris g
36	157.5	7.3	349	12	057408 meagris g
37	156.5	7.2	283	6	057408 meagris g
38	153.5	7.1	189	6	057408 meagris g
39	152.5	7.0	347	12	057408 meagris g
40	152.5	7.0	351	12	057408 meagris g
41	152	7.0	360	12	057408 meagris g
42	149.5	6.9	355	12	057408 meagris g
43	147.5	6.8	349	12	057408 meagris g
44	145	6.7	347	12	057408 meagris g
45	143.5	6.6	349	12	057408 meagris g

ALIGNMENTS

RESULT 1	ID	057408	PRELIMINARY:	PRT:	368 AA.
DT	01-JUN-1998	(TREMUR)	06, Created		
DT	01-JUN-1998	(TREMUR)	06, Last sequence update		
DT	01-MAR-2003	(TREMUR)	23, Last annotation update		
DE	Subgroup E ALV receptor				
OS	Meagris gallipavo (Common turkey)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.				
OX	NCBI_TaxID=9103;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-97471016; Pubmed-9326659;				
RA	Adkins H.B., Brojatsch J., Naughton J., Rolis M.M., Pesola J.M.,				
RA	Young J.A.;				
RT	"Identification of a cellular receptor for subgroup E avian leukosis				
RT	virus";				
RT	Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).				
RL	EMBL: AF006002; AAB93987.1;				
RS	HSSP: O14763; IDOG.				
DR	InterPro: IPR001450; 4Fe4S_ferredoxin.				
DR	InterPro: IPR000485; Death				
DR	InterPro: IPR001865; Ribosomal_S2.				
DR	InterPro: IPR001368; TNFR_c6.				
DR	Pfam: PF00531; death_1.				
DR	Pfam: PF00020; TNFR_c6; 2.				
DR	SMART: SM00208; TNFR; 1.				
DR	PROSITE: PS00198; 4Fe4S_FERREDOXIN; 1.				
DR	PROSITE: PS00117; DEATH_DOMAIN; 1.				
DR	PROSITE: PS00962; RIBOSOMAL_S2_1; 1.				
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.				
DR	PROSITE: PS00050; TNFR_NGFR_2; 2.				
DR	Receptor.				
SO	SEQUENCE				
Query Match	368 AA;	41020 MW;	5701AC2A6D4F87E2 CRC64;		
	22.5%;	Score 489;	DB 13;	Length 368;	

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:08:09 ; Search time 24 Seconds

(Without alignments)
805.332 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169
Sequence: 1 MEORGNAPASGARRKHP.....HLISGKFWYEGNADSAKS 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2135.5	98.5	440	1T10B_HUMAN	014763 homo sapien
2	1067	49.2	468	1T10A_HUMAN	000220 homo sapien
3	819.5	37.8	386	1T10D_HUMAN	09ubn6 homo sapien
4	595.5	27.5	381	1T10B_MOUSE	09qzr4 mus musculu
5	379.5	17.5	259	1T10C_HUMAN	014798 h tumor nec
6	264.5	12.2	471	1TR1A_BOVIN	019131 bos taurus
7	238.5	11.0	461	1TR1A_PIG	P50555 sus scrofa
8	210.5	9.7	455	1TR1A_HUMAN	P19438 homo sapien
9	209	9.6	454	1TR1A_MOUSE	P25148 mus musculu
10	192	8.9	327	1TNR6_MOUSE	093038 h tumor nec
11	191	8.8	417	1TNR6_HUMAN	P35445 homo sapien
12	189	8.7	335	1TNR6_HUMAN	P51867 bos taurus
13	186	8.6	323	1TNR6_BOVIN	P36941 homo sapien
14	179	8.3	435	1TNR3_HUMAN	P22934 rattus norv
15	175.5	8.1	461	1TR1A_RAT	077736 sus scrofa
16	171	7.9	332	1TNR6_PIG	063109 rattus norv
17	158	7.3	324	1TNR6_RAT	P18519 gallus gall
18	152	7.0	416	1TR16_CHICK	P20333 homo sapien
19	151.5	7.0	461	1TR1B_HUMAN	P03284 mus musculu
20	151	7.0	415	1TNR3_MOUSE	073559 compox viru
21	146.5	6.8	351	1CRMB_COMPX	092956 homo sapien
22	143.5	6.6	283	1TR1A_HUMAN	08uyar7 camelopox vi
23	143.5	6.6	349	1CRMB_CAMPS	000300 homo sapien
24	142.5	6.6	401	1T11B_HUMAN	P07174 rattus norv
25	142.5	6.6	425	1TR16_RAT	092041 mus musculu
26	142.5	6.6	427	1TR16_HUMAN	092041 mus musculu
27	141.5	6.5	417	1TR16_MOUSE	092041 mus musculu
28	138.5	6.4	349	1CRMB_VARV	008712 mus musculu
29	137	6.3	401	1T11B_MOUSE	P25119 mus musculu
30	135	6.2	474	1TR1B_MOUSE	09y66g homo sapien
31	135	6.2	616	1TR11_HUMAN	P15725 rattus norv
32	133.5	6.2	271	1TNR4_RAT	008727 rattus norv
33	133	6.1	401	1T11B_RAT	

34	132	6.1	180	1	TR22_MOUSE	09e62 mus musculu
35	131.5	6.1	272	1	TNR4_MOUSE	P47741 mus musculu
36	130	6.0	277	1	TNR5_HUMAN	P25942 homo sapien
37	128.5	5.9	1587	1	LMG3_HUMAN	09y666 homo sapien
38	125.5	5.8	1581	1	LMG3_MOUSE	09y666 mus musculu
39	124	5.7	176	1	TR23_MOUSE	09y666 mus musculu
40	124	5.7	498	1	TNR8_MOUSE	060846 mus musculu
41	122	5.6	300	1	TR6B_HUMAN	095407 homo sapien
42	122	5.6	326	1	VT2_MYXL	P29825 myxoma viru
43	122	5.6	595	1	TNR8_HUMAN	P28908 homo sapien
44	121.5	5.6	2813	1	VWF_CANFA	028295 canis famill
45	117	5.4	277	1	TNR4_HUMAN	P43489 homo sapien

ALIGNMENTS

RESULT 1	ID	TI0B_HUMAN	STANDARD:	PRT:	440 AA.
AC	014763	014720: 015508: 015517: 015531: 09BEVD;			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2)				
CN	TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
NP	SEQUENCE FROM N.A. (ISOFORM LONG), AND SEQUENCE OF N-TERMINUS.				
RC	TISSUE=ForeSkin fibroblast;				
RX	MEDLINE=974459925; PubMed=9311198;				
RA	Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bojani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Godwin R.G., Rauch C.T., "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";				
RT	EMBO J. 16:5386-5397(1997).				
RL	[2]				
RN	SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND ALTERNATIVE SPLICING.				
RP	MEDLINE=97431692; PubMed=9285725;				
RX	Creighton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.; "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";				
RT	Curr. Biol. 7:693-696(1997).				
RL	[3]				
RN	SEQUENCE FROM N.A. (ISOFORM LONG), AND CHARACTERIZATION.				
RP	TISSUE=Liver, and Spleen;				
RC	MEDLINE=98039016; PubMed=9373179;				
RX	Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschoep J.; "Characterization of two receptors for TRAIL.";				
RT	FEBS Lett. 416:329-334(1997).				
RL	[4]				
RN	SEQUENCE FROM N.A. (ISOFORM SHORT).				
RP	TISSUE=Ovary;				
RC	MEDLINE=97467719; PubMed=9326928;				
RX	Wu G.S., Burns T.F., McDonald E.R., III, Jiang W., Meng R., Krausz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.; "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";				
RT	Nat. Genet. 17:141-143(1997).				
RL	[5]				
RN	SEQUENCE FROM N.A. (ISOFORM SHORT).				
RP	MEDLINE=97390508; PubMed=9242610;				
RX	Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.; "An antagonist decoy receptor and a death domain-containing receptor				
RT					

RT for TRAIL.";
RL Science 277:815-818(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97467316; PubMed=9325248;
RA MacFarlane M., Ahmad M., Srinivasula S.M., Fernandes-Alnemri T.,
Cohen G.M., Alnemri E.S.;
RT "Identification and molecular cloning of two novel receptors for the
cytotoxic ligand TRAIL.";
RL J Biol. Chem. 272:25417-25420(1997).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=98090092; PubMed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunol. 7:821-830(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97390509; PubMed=9242611;
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M.,
Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.;
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy
receptors.";
RL Science 277:818-821(1997).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yasua Y.;
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2
gene in colorectal carcinoma.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX Cao X., Zhang W., Wan T.;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX Farrah T., Yu T., Gilbert T., Gross J., O'Hara P.;
RT "Homo sapiens homolog of tumor necrosis factor receptor.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX TISSUE=Cervix;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Umedin T.B., Teshlyuk S., Carninci P., Prange C.,
Rana S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.
RX MEDLINE=20017054; PubMed=10549288;
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullrich M., O'Connell M.,
Kelley R.F., Ashkenazi A., de Vos A.M.;
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
complex with death receptor 5.";
RL Mol. Cell 4:563-571(1999).

RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.
RX PubMed=10542098;
RA Mongkolkeha J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
Jones E.Y., Screaton G.R.;
RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
specificity in apoptotic initiation.";
RL Nat. Struct. Biol. 6:1048-1053(1999).
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFSL10/TRAIL. The
adaptor molecule FADD recruits caspase-8 to the activated
receptor. The resulting death-inducing signaling complex (DISC)
performs caspase-8 proteolytic activation which initiates the
subsequent cascade of caspases (aspartate-specific cysteine
proteases) mediating apoptosis. Promotes the activation of NF-
kappaB.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named Isoforms=2;
Name=Long; Synonyms=TRICK2B;
Isoid=014763-1; Sequence=Displayed;
Name=Short; Synonyms=TRICK2A;
Isoid=014763-2; Sequence=VSP_006490;
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;
very highly expressed in tumor cell lines such as HeLa S3, K562,
HL-60, SW480, A549 and G361; highly expressed in heart, peripheral
blood lymphocytes, liver, pancreas, spleen, thymus, prostate,
ovary, uterus, placenta, testis, esophagus, stomach and throughout
the intestinal tract; not detectable in brain.
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell
carcinoma of the head and neck.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 1 death domain.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF016849; AAC51778.1; -
DR EMBL; AF018657; AAB70577.1; -
DR EMBL; AF018658; AAB70578.1; -
DR EMBL; AF016266; AAB81160.1; -
DR EMBL; AF022386; AAB71949.1; -
DR EMBL; AF020501; AAB71412.1; -
DR EMBL; AF016268; AAC01565.1; -
DR EMBL; AF012535; AAB67103.1; -
DR EMBL; AB014718; BAA33723.1; -
DR EMBL; AB014710; BAA33723.1; JOINED.
DR EMBL; AB014711; BAA33723.1; JOINED.
DR EMBL; AB014712; BAA33723.1; JOINED.
DR EMBL; AB014713; BAA33723.1; JOINED.
DR EMBL; AB014714; BAA33723.1; JOINED.
DR EMBL; AB014715; BAA33723.1; JOINED.
DR EMBL; AB014716; BAA33723.1; JOINED.
DR EMBL; AF153687; AAF75567.1; -
DR EMBL; AF192548; AAF07175.1; -
DR EMBL; BC001281; AAH01281.1; -
DR PDB; 1D0G; 22-OCT-99.
DR PDB; 1D4V; 01-NOV-99.
DR Genew; HGNC:11905; TNFRSF10B.
DR MIM; 603612; -
DR MIM; 601400; -
DR GO; GO:0016021; C:Integral to membrane; IC.
DR GO; GO:0016506; F:apoptosis activator activity; NAS.
DR GO; GO:0008656; F:caspase activator activity; NAS.
DR GO; GO:0004872; F:receptor activity; NAS.

Query Match 98.5%; Score 2135.5; DB 1; Length 440;
 Best Local Similarity 93.0%; Pred. No. 3,3e-152;
 Matches 409; Conservative 0; Mismatches 2; Indels 29; Gaps 1;

QY 1 MEORGNAPPAASGARRRHGGPREARGARGLRVPYTLVVAALLVSAESALITQOD 60
 1 MEORGNAPPAASGARRRHGGPREARGARGLRVPYTLVVAALLVSAESALITQOD 60
 DB 1 MEORGNAPPAASGARRRHGGPREARGARGLRVPYTLVVAALLVSAESALITQOD 60
 QY 61 LAPOQAAAPQOKSSSEGLCPGGHHISEGRCISCKGQDYSTMNDLLFCLRTCD 120
 61 LAPOQAAAPQOKSSSEGLCPGGHHISEGRCISCKGQDYSTMNDLLFCLRTCD 120
 DB 61 LAPOQAAAPQOKSSSEGLCPGGHHISEGRCISCKGQDYSTMNDLLFCLRTCD 120
 QY 121 SGEVEISPTCTTNTNTYCCCEGFEEDSPKRCRTGCGPRGMVVGDCPTMSDIECV 180
 121 SGEVEISPTCTTNTNTYCCCEGFEEDSPKRCRTGCGPRGMVVGDCPTMSDIECV 180
 DB 121 SGEVEISPTCTTNTNTYCCCEGFEEDSPKRCRTGCGPRGMVVGDCPTMSDIECV 180
 QY 181 KE-----SGIIGTVAAVAVLVAVFVCKSLMKVY 211
 181 KE-----SGIIGTVAAVAVLVAVFVCKSLMKVY 211
 DB 181 KEGTSHSGEAPAVEETVTSPTGPASPCSLSGIIGTVAAVAVLVAVFVCKSLMKVY 240
 QY 212 LPTLKICSGGGDPERVDRSSORPGADENVLNEIYSIIQPTVPEQEMVQPAEPTGV 271
 212 LPTLKICSGGGDPERVDRSSORPGADENVLNEIYSIIQPTVPEQEMVQPAEPTGV 271
 DB 241 LPTLKICSGGGDPERVDRSSORPGADENVLNEIYSIIQPTVPEQEMVQPAEPTGV 300
 QY 272 NMLSPGESEHLEPAEERSQRRLVPAENEGDPTLRCQCFDFADLVFDSMEPLMRK 331
 301 NMLSPGESEHLEPAEERSQRRLVPAENEGDPTLRCQCFDFADLVFDSMEPLMRK 360
 DB 332 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 391
 361 LGLMDEIVKAAEAAGHDTLYMLIKVNTKGRDASVHTLLDALETIGERLAKOIED 420
 QY 392 HLSSGKFWYLEGNNADSAYS 411
 421 HLSSGKFWYLEGNNADSAYS 440
 DB 421 HLSSGKFWYLEGNNADSAYS 440

RESULT 2
 T10A_HUMAN
 ID T10A_HUMAN STANDARD; PRT; 468 AA.
 AC 000220; Q96662;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 10A precursor (Death
 receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL
 receptor 1) (TRAIL-R1).
 GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97238921; PubMed=9082980;
 RA Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Ebner R., Ni J.,
 Dixit V.M.;
 RT "The receptor for the cytotoxic ligand TRAIL.";
 RL Science 276:111-113(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Dlatkovic L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Urdin T.B., Toshiyuki S., Canninci P., Plange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Rahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
 Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=98090092; PubMed=9430227;
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
 FADD-dependent apoptosis and activate the NF-kappaB pathway.";
 RL Immunity 7:821-830(1997).
 CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. The
 adaptor molecule FADD recruits caspase-8 to the activated
 receptor. The resulting death-inducing signaling complex (DISC)
 performs caspase-8 proteolytic activation which initiates the
 subsequent cascade of caspases (aspartate-specific cysteine
 proteases) mediating apoptosis. Promotes the activation of NF-
 kappaB.
 CC -!- SUBUNIT: Can interact with TRADD and RIP.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Widely expressed. High levels are found in
 spleen, peripheral blood leukocytes, small intestine and thymus,
 but also in K562 erythroleukemia cells, MCF7 breast carcinoma
 cells and activated T-cells.
 CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 1 death domain.

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 CC -----
 DR EMBL: U90875; AAC5126.1; -;
 DR EMBL: BC012866; AAH12866.1; -;
 DR HSSP: O14763; 1D0G; TNFRSF10A.
 DR Genew; HENC:11904; TNFRSF10A.
 DR MIM: 603611; -;
 DR GO: GO:0016021; C:integral to membrane; IC.
 DR GO: GO:0016506; F:apoptosis activator activity; NAS.
 DR GO: GO:0008656; F:caspase activator activity; NAS.
 DR GO: GO:0005035; F:death receptor activity; TAS.
 DR GO: GO:0004872; F:receptor activity; NAS.
 DR GO: GO:0045569; F:TRAIL binding activity; NAS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
 DR GO: GO:0006919; P:caspase activation; NAS.
 DR GO: GO:0008625; P:induction of apoptosis via death domain rec. .; NAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR00488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 2.
 DR PROSITE: PSS0017; DEATH_DOMAIN; 1.
 DR PROSITE: PSS0052; TNFR_NGR_1; 2.
 DR PROSITE: PSS0050; TNFR_NGR_2; 2.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 468
 FT DOMAIN 24 239
 FT TRANSSEM 240 262
 FT DOMAIN 263 468
 CYTOPLASMIC (POTENTIAL).
 TUMOR NECROSIS FACTOR RECEPTOR
 SUPPLEMENTARY MEMBER 10A.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.


```

FT DISULFID 118 131 BY SIMILARITY.
FT DISULFID 121 139 BY SIMILARITY.
FT DISULFID 141 155 BY SIMILARITY.
FT DISULFID 158 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 35 35 P -> S (IN TRAIL-R4-B).
FT VARIANT 310 310 /FTID=VAR.011417.
FT VARIANT 310 310 S -> L (IN TRAIL-R4-B).
FT FT /FTID=VAR.011418.
SQ SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;

Query Match 37.8%; Score 819.5; DB 1; Length 386;
Best Local Similarity 43.7%; Pred. No 5.4e-54;
Matches 193; Conservative 36; Mismatches 116; Indels 97; Gaps 5;

QY 5 GONAPASGARKRHGPGPREARGAPGLRVPKTL-VLVVAVALLVSAESALITQODLA 62
5 GQSVTPASSARAGRYPCARTASGRPWLDPKILKEVVFIVAVLLPVVDASATIPRDEV 64
D6 63 PQORAPQOKRSPSEGLCPGHHISFDGDCISCKGODYSTHMDLFLCRLCTRCDG 122
65 PQOTVAPQOQRRSLKEECPAGSHRSEYTGACNPCTEGVDYTTASNNLPSCLLCTYCKSG 124
QY 123 EVELSPCTTRNTVCOCEGTFREEDSPEMCRKCRGPGMWKVGDCPTMWDIECVHKE 182
125 QTKKSSCTTRDRVCOCEGTFREEDSPEMCRKCRGPGMWKVGDCPTMWDIECVHKE 184
QY 183 SGIIIGTVAA-----VVLIIVAFYCKSLMKKVLPLYKGC 219
185 AASSTGTPAAEEVTTILGLMASPYHYLIIVLVLLVAVVGFSCRKFTSYLKGIC 244
QY 220 SGGGSGPERDR-----SSORPGAEADVLAIEYS--ILQTPVPEQEMEQEPAPPT 269
245 SGGGSGPERDR-----SSORPGAEADVLAIEYS--ILQTPVPEQEMEQEPAPPT 304
QY 270 GYVNLSPGSEHLEPAEARSORRLVPAWGDPETLRQCFDDPADVLPPDSWPLM 329
305 GYVNLSPGSEHLEPAEARSORRLVPAWGDPETLRQCFDDPADVLPPDSWPLM 339
D6 330 RKLGLMDEIKVAKAEGAHRDLYTMLIKVWKTGRDASVHLLDALLETGERLAKOKI 389
340 RKLGLMDEIKVAKAEGAHRDLYTMLIKVWKTGRDASVHLLDALLETGERLAKOKI 362
QY 390 EDHLLSGKPMYLEGNADSAXS 411
363 QDOLVSGEKLFEDEGSAFS 384

RESULT 4
ID T10B_MOUSE STANDARD; PRT: 381 AA.
AC Q9QZM4; Q9JUL5; Q9JUL6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (MK).
GN TNFRSF10B OR DR3 OR KILLER.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerogamathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=99310501; Pubmed=10383128;
RA "Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S., Molecular cloning and functional analysis of the mouse homologue of the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand (TRAIL) death receptor."
RT Cancer Res. 59:2770-2775(1999).

```

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RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Nakamura Y., Tamari M., Watanabe O.;
RT "Mouse TRAIL receptor."
CC Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for the cytotoxic ligand TNFRSF10/TRAIR. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Promotes the activation of NF-kappaB.
CC -1- SUBUNIT: Homotrimer. Can interact with TRADD and RIP (by similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in heart, lung and kidney.
CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -1- SIMILARITY: Contains 1 death domain.
CC -----
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CC -----
DR EMBL: AF176833; AAD52656.1;
DR EMBL: AB031081; BAA96462.1;
DR EMBL: AB031082; BAA96463.1;
DR HSP: O14763; 1D0G.
DR MG: MG1:1341090; Tnfrsf10b.
DR InterPro: IPR000488; Death.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; TNFR_c6; 2.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Transmembrane; Repeat; Signal.
FT SIGNAL 1 52
FT CHAIN 53 381
FT DOMAIN 53 160
FT TRANSMEM 161 181
FT DOMAIN 182 381
FT REPEAT 26 86
FT REPEAT 87 129
FT REPEAT 130 169
FT DOMAIN 273 356
FT DISULFID 74 85
FT DISULFID 88 105
FT DISULFID 108 121
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FT DISULFID 131 145
FT DISULFID 148 161
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FT CONFLICT 42 42
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FT CONFLICT 229 229
FT CONFLICT 306 306
SQ SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;

Query Match 27.5%; Score 595.5; DB 1; Length 381;
Best Local Similarity 35.6%; Pred. No. 2.8e-37;

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FT	REPEAT	192	206	3
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FT <td>REPEAT</td> <td>222</td> <td>236</td> <td>5</td>	REPEAT	222	236	5
FT <td>DISULFID</td> <td>53</td> <td>66</td> <td>BY SIMILARITY.</td>	DISULFID	53	66	BY SIMILARITY.
FT <td>DISULFID</td> <td>69</td> <td>85</td> <td>BY SIMILARITY.</td>	DISULFID	69	85	BY SIMILARITY.
FT <td>DISULFID</td> <td>88</td> <td>101</td> <td>BY SIMILARITY.</td>	DISULFID	88	101	BY SIMILARITY.
FT <td>DISULFID</td> <td>91</td> <td>109</td> <td>BY SIMILARITY.</td>	DISULFID	91	109	BY SIMILARITY.
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FT <td>DISULFID</td> <td>128</td> <td>141</td> <td>BY SIMILARITY.</td>	DISULFID	128	141	BY SIMILARITY.
FT <td>DISULFID</td> <td>131</td> <td>149</td> <td>BY SIMILARITY.</td>	DISULFID	131	149	BY SIMILARITY.
FT <td>LIPID</td> <td>236</td> <td>236</td> <td>GPI-ANCHOR (POTENTIAL).</td>	LIPID	236	236	GPI-ANCHOR (POTENTIAL).
FT <td>CARBOHYD</td> <td>77</td> <td>77</td> <td>N-LINKED (GLCNAC. . .) (HIGH MANNOSE)</td>	CARBOHYD	77	77	N-LINKED (GLCNAC. . .) (HIGH MANNOSE)
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FT <td>CARBOHYD</td> <td>156</td> <td>156</td> <td>N-LINKED (GLCNAC. . .) (HIGH MANNOSE)</td>	CARBOHYD	156	156	N-LINKED (GLCNAC. . .) (HIGH MANNOSE)
FT <td>CONFLICT</td> <td>119</td> <td>119</td> <td>E -> V (IN REF. 5).</td>	CONFLICT	119	119	E -> V (IN REF. 5).
FT <td>SEQUENCE</td> <td>259 AA:</td> <td>27395 MW:</td> <td>FEBBF7FCEAAE50B8 CRC64:</td>	SEQUENCE	259 AA:	27395 MW:	FEBBF7FCEAAE50B8 CRC64:
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	Best Local Similarity	51.7%;	Pred. No. 2.4e-21;	
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Oy	33	RVPKTL-VLVVAVNLLVSAESALITOODLAPQORAPQOKRRSPSEGLCPGGHISD	90	
Db	3	RIPKTLKFEVIVVAVLPLEVLAVSATTAQEEVPOOTVAPOQORHSFGKECPAGSHRSEH	62	
Oy	91	GRDCISCRSGYGDYSYHMMDDLFLCLRCTGDSGEVLELSPCTTRNTVCOEECTPREDSF	150	
Db	63	TGACNPFCTEGVDYTIASNNBSCFPCTCYCKSSQDKRKSSCTMTIDYVCOCKEGBTFRENSP	122	
Oy	151	EMCRKCRTPGPRGMYKVGDCCTPMSDIECVHK	181	
Db	123	EMCRKRC-SRCPSSGEVOVSNCSTMSDDICVEE	152	
RESULT 6				
TRIA_BOVIN	STANDARD:	PRT:	471 AA.	
AC	019131:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)			
DE	(TNF-RI) (TNF-RI) (p55).			
GN	TNFRSF1A OR TNFR1.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	NCBI_TaxID=9913;			
RR	SEQUENCE FROM N.A.			
RC	TISSUE=Arteria;			
RX	MEDLINE=96273505; PubMed=9613449;			
RA	Lee E.-K., Kehrl M.E. Jr., Taylor M.J.;			
RT	"Cloning and sequencing of cDNA encoding bovine tumor necrosis factor			
RT	(TNF)-receptor I.";			
RU	Vet. Immunol. Immunopathol. 61:379-385(1998).			
CC	-I- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric			
CC	TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits			
CC	signaling complex (DISC) performs caspase-8 proteolytic activation			
CC	which initiates the subsequent cascade of caspases (aspartate-			
CC	specific cysteine proteases) mediating apoptosis (By similarity).			
CC	-I- SUBUNIT: Binding of TNF to the extracellular domain leads to			
CC	homotrimerization. The aggregated death domains provide a novel			
CC	molecular interface that interacts specifically with the death			
CC	domain of TRADD. Various TRADD-interacting proteins such as FRRAS,			
CC	RIP and possibly FADD, are recruited to the complex by their			
CC	association with TRADD. This complex activates at least two			
CC	distinct signaling cascades, apoptosis and NF-kappa-B signaling.			

CC		- binds BAG4 (by similarity).
CC	-1-	SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1-	SIMILARITY: Contains 4 TNFR-Cys repeats.
CC	-1-	SIMILARITY: Contains 1 death domain.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or_send_an_email_to_license@sib-sib.ch).
CC		-----
DR	EMBL; U90937;	AAB65143.1; .
DR	HSSP; P19438;	TNFR.
DR	InterPro; IPR000488;	Death.
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DR	Pfam; PF000531;	death_1.
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DR	SMART; SMO0208;	TNFR_NGFR_1; 3.
DR	PROSITE; PS00652;	TNFR_NGFR_2; 3.
DR	PROSITE; PS00500;	TNFR_NGFR_2; 3.
DR	PROSITE; PS00017;	DEATH_DOMAIN; 1.
KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	
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FT		POTENTIAL.
FT		TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 1A.
FT	DOMAIN	22..210
FT	TRANSMEM	211..233
FT	DOMAIN	234..471
FT	REPEAT	43..82
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FT	REPEAT	126..166
FT	REPEAT	167..195
FT	DOMAIN	340..360
FT	DOMAIN	372..457
FT	DISULFD	44..58
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FT	DISULFD	62..81
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FT	DISULFD	146..158
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FT	DISULFD	185..190
FT	CARBOHYD	54..55
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FT	CARBOHYD	151..151
SO	SEQUENCE	471 AA; 51367 MW; 5243EFS1ADEBIC4 CXC64;
Query Match		12.2%; Score 264.5; DB 1; Length 471;
Best Local Similarity		24.5%; Pred. No. 1.9e-12;
Matches 117; Conservative	52; Mismatches 183; Indels 125; Gaps 23;	
QY	30	PGLRPKPLVAVVAAYLLVLAESFLITQQDLAPQQAAPQAKSSPSSEG-----CPPG 84
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QY	85	HHISED-----GR--DCISCRTGYODSTHMNDLCLRCTRC--VSGEVELSPCTTTNTTV 136
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QY	137	QCCEEGFRE--EDSPENCRCRTGCCPGMNVGDCTPMSDIECVHKESGIII----- 187
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QY	188	-----GYTAAVAVLIY-----AVFGSKSLMKKV 211
DB	182	CHDCKNKCEERLCPTRPSTGSDOPGTGVTLVLPVIVGLCLASFASVYLACRYQRNK-- 239

QY 212 LPYLKICSGGG-----GDERVDRS-----SORPGADNVLNEIVS----- 248
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 QY 249 -LIQPIOV-----PEQEMEVOEPAPETGVNMLSPG--ESEHLLPEAEERS 291
 Db 299 AVASPSSEETAPPHLKAGPILPGPPASTHLCTPGPPASTHLCTPGPPASTHLCTPVQKWEA 358
 QY 292 QRRRLVPAPEGDEPTETLRQCFDFALVPDSEWEPRLKGLMDNITKAKAEAGH-R 350
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RESULT 7
 ID TRIA_PIG STANDARD; PRT; 461 AA.
 AC P50555;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 GN (TNF-R1) (TNF-R1) (p55).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID:9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96011645; PubMed=7590278;
 RA Suter B., Pauli U.H.;
 RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.";
 RL Gene 163:263-266(1995).
 CC -1- FUNCTION: Receptor for TNFRSF2/TNF-alpha and homotrimeric TNFRSF1/lymphotoxin alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFs, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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 CC
 CC EMBL, U19994; AAC48499.1; .
 DR PIR, JC4302; JC4302.
 DR HSSP, P19438; 1YNR.
 DR InterPro, IPR000488; Death.
 DR InterPro, IPR001368; TNFR_c6.
 DR Pfam, PF00531; death_1.
 DR Pfam, PF00020; TNFR_c6; 3.

DR SMART, SM00005; DEATH; 1.
 DR SMART, SM00208; TNFR; 4.
 DR PROSITE, PS00652; TNFR_NGFR.1; 3.
 DR PROSITE, PS00650; TNFR_NGFR.2; 2.
 DR PROSITE, PS0017; DEATH_DOMAIN; 1.
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 DR K

RESULT 8
ID TRIA_HUMAN STANDARD: PRT: 455 AA.
AC P19438:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55) (CD120a) [Contains: Tumor necrosis factor
binding protein 1 (TRAF1)].
GN TNFRSF1A OR TNFR1 OR TNFRAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=90235285; PubMed=2158863;
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Mong G.H.W.,
RA Geranaga T., Granger G.A., Lentz R., Raab H., Kohr W.J., Goeddel D.V.;
RT "Molecular cloning and expression of a receptor for human tumor
necrosis factor.";
RL Cell 61:361-370(1990).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235284; PubMed=2158862;
RA Loetscher H., Pan Y.-C.E., Lamm H.-W., Gentz R., Brockhaus M.,
RA Tabuchi H., Lesslauer W.;
RT "Molecular cloning and expression of the human 55 kd tumor necrosis
factor receptor.";
RL Cell 61:351-359(1990).
[3]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 41-53; 110-124 AND 199-201.
RX MEDLINE=91006021; PubMed=1698610;
RA Nopfer Y., Kemper O., Brakebusch C., Engelmann H., Zwang R.,
RA Aderka D., Holtmann H., Wallach D.;
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA
for the type I TNF-R, cloned using amino acid sequence data of its
soluble form, encodes both the cell surface and a soluble form of the
receptor.";
RL EMBO J. 9:3269-3278(1990).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91090841; PubMed=1702293;
RA Himmler A., Nauber-Fogy I., Kroenke M., Scheurich P., Pfitzenmaier K.,
RA Lantzi M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
factor receptor chain (p60) and its soluble derivative, tumor
necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
[5]
RP SEQUENCE FROM N.A.
RP TISSUE-Placenta;
RX MEDLINE=91017509; PubMed=2170974;
RA Grey P.W., Barrett K., Chantry D., Turner M., Feldman M.;
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and
expression of recombinant soluble TNF-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).
[6]
RP SEQUENCE FROM N.A.
RX MEDLINE=92250049; PubMed=131517;
RA Fuchs P., Stehl S., Dworak M., Himmler A., Ambros P.F.;
RT "Structure of the human TNF receptor I (p60) gene (TNFR1) and
localization to chromosome 12p13.";
RL Genomics 13:219-224(1992).
[7]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N.R., Toch E.J., Yi Q., Nickerson D.A.;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
[8]
RP SEQUENCE FROM N.A.

RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshlyak S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Halys S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[9]
RP SEQUENCE OF 41-45.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
urine. Evidence for immunological cross-reactivity with cell surface
tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
[10]
RP INTERACTION WITH BAGA.
RX MEDLINE=99115917; PubMed=9915703;
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
death domains.";
RL Science 283:543-546(1999).
[11]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Loetscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
beta complex: implications for TNF receptor activation.";
RL Cell 73:431-445(1993).
[12]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
RX MEDLINE=97094982; PubMed=8939750;
RA Naismith J.H., Devine T.O., Khono H., Sprang S.R.;
RT "Structures of the extracellular domain of the type I tumor necrosis
factor receptor.";
RL Structure 4:1251-1262(1996).
[13]
RP VARIANTS FHF ARG-59; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.
RX MEDLINE=99213501; PubMed=10199409;
RA McDermott M.F., Aksentjevich I., Galon J., McDermott E.M.,
RA Ogunkolade B.W., Centola M., Mansfield E., Gadinia M., Karenko L.,
RA Petersson T., McCarthy J., Frucht D.M., Ainger M., Torosyan Y.,
RA Teppo A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G.,
RA Schliengen R., Kumarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,
RA Mulvey J., Quane K.A., Molloy M.G., Rnati A., Powell R.J.,
RA Hitman G.A., O'Shea J., Kastner D.L.;
RT "Germline mutations in the extracellular domains of the 55 kDa TNF
receptor, TNFR1, define a family of dominantly inherited
autoinflammatory syndromes.";
RL Cell 97:133-144(1999).
[14]
RP FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
TNFSF1/lymphotxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
signaling complex (DISC) performs caspase-8 proteolytic activation
which initiates the subsequent cascade of caspases (aspartate-
specific cysteine proteases) mediating apoptosis. Contributes to
the induction of noncytotoxic TNF effects including anti-viral

CC state and activation of the acid sphingomyelinase.
 CC - SUBUNIT: Binding of TNF to the extracellular domain leads to
 CC homotrimerization. The aggregated death domains provide a novel
 CC molecular interface that interacts specifically with the death
 CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 CC RIP and possibly FADD, are recruited to the complex by their
 CC association with TRADD. This complex activates at least two
 CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4.
 CC SUBCELLULAR LOCATION: Type I membrane protein and secreted.
 CC - DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO
 CC THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH
 CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
 CC - PTM: The soluble form is produced from the membrane form by
 CC proteolytic processing.
 CC - DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant
 CC familial hibernian fever (FHF), a disease characterized by
 CC recurrent fever, abdominal pain, localized tender skin lesions and
 CC myalgia.
 CC - SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC - SIMILARITY: Contains 1 death domain.
 CC - DATABASE: NAME=PROW; NOTE=CD guide CD120a entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120a.htm".
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X55313; CAA39021.1; -
 DR EMBL: M33294; AAA03210.1; -
 DR EMBL: M58286; AAA36753.1; -
 DR EMBL: M63121; AAA36754.1; -
 DR EMBL: M73866; AAA61201.1; -
 DR EMBL: M75865; AAA61201.1; JOINED.
 DR EMBL: M60275; AAA36756.1; -
 DR EMBL: A21522; CAA01558.1; -
 DR EMBL: A131997; AAM77802.1; -
 DR EMBL: BC010140; AAH10140.1; -
 DR PIR: A38208; GQH0T1.
 DR PDB: ITNR: 31-JUL-94.
 DR PDB: INCF: 07-DEC-95.
 DR PDB: LEXT: 11-JAN-97.
 DR PDB: IFT4: 12-OCT-01.
 DR PDB: IICH: 01-APR-02.
 DR Genew: HGNC:11916; TNFRSF1A.
 DR MIM: 191190; -
 DR MIM: 142680; -
 DR GO: GO:0005576; C:extracellular; TAS.
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0005033; F:tumor necrosis factor receptor, type I actl. .; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 Query Match 9.7%; Score 210.5; DB 1; Length 455;
 Best Local Similarity 22.5%; Pred. No. 2e-08;
 Matches 104; Conservative 60; Mismatches 160; Indels 139; Gaps 22;
 QY 34 VPKTVLVVAANVLLVSAESALITQODLAPQORAPQOKRSSPSGLCPPHIHIEDGR- 92
 DB 6 VPDLLPLVLELLVLTGIRSGVI--GLVP--HLGDRKRKDS---VPOGKYTHPQUNNS 56
 QY 93 -----DCISCKYGDYSTHWNDDLFCLACTRC--DSGEVLS 127
 DB 57 ICTCTKHGTYLYNDPCPGQDTPDCEGSG-SFTASFNHLRHCLSCSKCKREMQVEIS 115
 QY 128 PCTTTRNVCOCEESTFREEDSPEM-----CRKCTG-----CPRG-WVK 166
 DB 116 SCTVDRDVTGCGCRKNQYRHYWSENLFQCFNCSLCLNGTVHLSCKOEKONTVCTCHAGFELR 175

QY 167 VDCPTWSD-----IEC-----VHKESGIIIGVTAAVVLIVAVFC-KSL----- 207
 DB 176 ENECSCSKCKSLECTLCPLQIENWKGTFDSGTVLLPLVIFGCLLSLPLGLMYR 235
 QY 208 ---WKVLPYLKIGTCSGGGDPER---VDRSSQPGADNVLNETHVSILQPTQPEOME 261
 DB 236 YQRMKSLYSI--VC--GKSTPEKEGELEGTTRPLAENPFSFP-----TPGFTPLGFS 286
 QY 262 VOEPAEPGVNMLSPGSEHLELPEAERSRRLIYVANG-----DPTETLR 310
 DB 287 PVPSSTFYSSSTYTPGDCPNRAP-----RREVAPEYGGADPILATALASDTPNPL 338
 QY 311 QCFDFA-----DLVPFDSMEPLMKRLGMDNEI-KVAKAABAAGHRD 351
 DB 339 QKMEDSAHKPSQSLDTPDPAITYAVENPPLRWKEFVARLDSBHEIDRLQNGRCIRE 398
 QY 352 TLYTMLIKWVKT-----GRDASVHLLDALFTLGERL 384
 DB 399 AQYSMLATWRRRTTREPREATLEILGRVLRDMDLGLCTEDIEBAL 441
 RESULT 9
 ID TRIA_MOUSE STANDARD: PRT: 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)
 DE (TNF-R1) (p55).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.,
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fiswick D.A., Cope A.P., Kisonoghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.,
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX TISUE=Spieen;
 MEDLINE=92039815; PubMed=1657766;
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.,
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94245292; PubMed=8188324;
 RA Bebo B.F., Linthicum D.S.,
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";

RL Immunogenetics 39:450-451(1994).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93156721; PubMed-8381516;
 RA Roth J., Bluetmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175(1993).
 [7]
 RN SEQUENCE FROM N.A.
 RP MEDLINE-22368257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL -1- FUNCTION: Receptor for TNFR2/TNF-alpha and homotrimeric
 TNFR1/Lymphotoxin-alpha. The adaptor molecule FADD recruits
 caspase-8 to the activated receptor. The resulting death-activation
 signaling complex (DISC) performs caspase-8 proteolytic activation
 which initiates the subsequent cascade of caspases (aspartate-
 specific cysteine proteases) mediating apoptosis (By similarity).
 CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
 homotrimerization. The aggregated death domains provide a novel
 molecular interface that interacts specifically with the death
 domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 RIP and possibly FADD, are recruited to the complex by their
 association with TRADD. This complex activates at least two
 distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 CC Binds BAG4 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M60468; AAA39751.1; -
 DR EMBL: M59377; AAA40464.1; -
 DR EMBL: X59238; CAA41922.1; -
 DR EMBL: X57796; CAA40936.1; -
 DR EMBL: L26349; AAA59361.1; -
 DR EMBL: M76656; AAA40465.1; -
 DR EMBL: M88067; AAA40465.1; JOINED.
 DR EMBL: M76655; AAA40465.1; JOINED.
 DR EMBL: BC004599; AAH04599.1; -
 DR HSP: A38634; GOMST1.
 DR HSP: P19438; 1EXT.
 DR MGD: MGI:1314884; Tnfrsf1a.
 DR GO: GO:0001766; P:cell surface receptor linked signal transdu. . .; IMP.
 DR GO: GO:0006952; P:defense response; IMP.
 DR GO: GO:0006954; P:inflammatory response; IMP.
 DR GO: GO:0007515; P:lymph gland development; IMP.

DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 3.
 DR PROSITE: PS0017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 454
 FT
 FT DOMAIN 22 212
 FT TRPMEM 213 235
 FT DOMAIN 236 454
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 339 349
 FT DOMAIN 356 441
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 195
 FT CARBOHYD 185 191
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 202 202
 FT CONFLICT 394 394
 SQ
 Query Match 454 AA; 50129 MW; 0710C2BEC3C2BBD9 CRC64;
 Best Local Similarity 9.6%; Score 209; DB 1; Length 454;
 Matches 105; Conservative 58; Mismatches 137; Indels 188; Gaps 24;
 31 GLRVPRTIVYVNAVILVLSAASALTQODLAQQAAPQKSSPSEGLCPGCHH1--- 87
 2 GLPTVGLLSTLVLLDLMLGTHPSGV1--GLVPS--LGDERKDS---LCPGKTVHSHK 53
 88 -----SEDGRD--CISCKRGQDYSTHWNLDLFLCLRCTRC--DSGEV 124
 54 NNSICCTGCHKGYLVSDCPSPGRDVCRCENG-FTASQNYLRCLCKTKRKEMSQV 112
 125 ELSPCTTNTNTVQCCEBGFREEDSPM-----CRKCRFG-----CPRG- 163
 113 EISPCADKKTVCCKENOFORYLSETHFOCVDCSCFNGTVTIPCKETQNTVCNCHAGF 172
 164 MVKVGDCSTPS-----DIECH-----KESG-----IIGVYAAAVLV 198
 173 FLRESBVCPSHCKKNECKKLCPLPLNVTNPQSGTAVLLPLVILGLCLSTFT- 231
 199 AVFVCKSLMLKKVLPYLKIGSGGGDPERVDRSSORPGAEDNVLEIVSILOPTVPQC 258
 232 -SLMCRPRV-----RP-----EVSIIORDVPVK 256
 259 EMEVQEPAP-----TGVN-----MSPGSE-----HLEPAEAE 289
 257 EERAGRPPLTPAPSPAPSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPGSPG 315
 290 RSQRRRLVYANGD-----PTETLRQCFDFA-----DLVPE 322
 316 -----VPTGADPLVESLCSVPAPTSVQKWEBSAHPQRPDNDALIVAVVGVP 368
 323 DSWEPLMRKGLMDNET-KVAKAEAGHRDTLTMLIKWNKGRDASVHTLLDAETLG 381

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DB      369  ARWKEFRFMGLSEHIERLEEMQNGRCJREAOYSMLTEAWRRRTPRHE-----DTLEVVG 422
OY      382  ERLAKOKI 389
DB      423  LVLSKMMN 430

RESULT 10
TNRF6_MOUSE STANDARD: PRT: 327 AA.
ID      TNRF6_MOUSE
AC      P25446; O8DCQ1;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE      receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE      (CD95).
CN      TNFRSF6 OR APT1 OR FAS.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92148151; PubMed=1371136;
RA      Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA      Copeland N.G., Jenkins N.A., Nagata S.,
RT      "The CDNA structure, expression, and chromosomal assignment of the
RT      mouse Fas antigen."
RL      J. Immunol. 148:1274-1279(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=129/SV;
RA      Koczan D., Ibrahim S.M., Thiesen H.J.;
RT      "Role of a mutant fas receptor in a transgenic mouse."
RT      Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      STRAIN=C57BL/6J; TISSUE=Kidney;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA      Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nakado T., Pesole G., Quackenbush J.,
RA      Schramm L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momchales P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Winking L.,
RA      Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection."
RT      Nature 409:685-690(2001).
RN      [4]
RP      SEQUENCE OF 1-96 FROM N.A.
RX      MEDLINE=93189576; PubMed=7680478;
RA      Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT      "Aberrant transcription caused by the insertion of an early
RT      transposable element in an intron of the Fas antigen gene of lpr
RT      mice."
RT      Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN      [5]
RP      INTERACTION WITH DAXX.
RX      MEDLINE=97358533; PubMed=9215629;
RA      Yang X., Khosravi-Far R., Chang H.Y., Baltimore D.;

```

```

RT      "Daxx, a novel Fas-binding protein that activates JNK and apoptosis."
RT      Cell 89:1067-1076(1997).
RN      [6]
RP      VARIANT LPR.
RX      MEDLINE=92195401; PubMed=1372394;
RA      Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA      Nagata S.;
RT      "Lymphoproliferation disorder in mice explained by defects in Fas
RT      antigen that mediates apoptosis."
RL      Nature 356:314-317(1992).
CC      -i- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
CC      recruits caspase-8 to the activated receptor. The resulting death-
CC      inducing signaling complex (DISC) performs caspase-8 proteolytic
CC      activation which initiates the subsequent cascade of caspases
CC      (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC      mediated apoptosis may have a role in the induction of peripheral
CC      tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC      both (By similarity).
CC      -i- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC      -i- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -i- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC      LIVER, LUNG, HEART, AND ADULT OVARY.
CC      -i- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC      AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC      -i- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC      DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC      PRODUCTION.
CC      -i- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC      -i- SIMILARITY: Contains 1 death domain.
CC      -----
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CC      -----
DR      EMBL: M83649; AAA37593.1; -
DR      EMBL: AK002590; BAB22211.1; -
DR      EMBL: AJ285702; CAC00638.1; -
DR      EMBL: AJ285703; CAC00638.1; JOINED.
DR      EMBL: AJ295704; CAC00638.1; JOINED.
DR      EMBL: S56490; AAB25700.1; -
DR      EMBL: S56485; AAB25700.1; JOINED.
DR      EMBL: S56486; AAB25700.1; JOINED.
DR      PIR: A46484; A46484.
DR      HSSP: P25445; IDDF.
DR      GSD: MG1:95484; TNFRsf6.
DR      InterPro: IPR000488; Death.
DR      InterPro: IPR001368; TNFR_c6.
DR      Pfam: PF00531; death.1.
DR      Pfam: PF00020; TNFR_c6; 3.
DR      SMART: SM00005; DEATH; 1.
DR      SMART: SM00208; TNFR; 3.
DR      PROSITE: PS00652; TNFR_NGFR.1; 2.
DR      PROSITE: PS50050; TNFR_NGFR.2; 2.
DR      PROSITE: PS50017; DEATH_DOMAIN; 1.
KW      Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal;
KW      Disease mutation.
FT      SIGNAL 1 21
FT      CHAIN 22 327
FT      DOMAIN 22 169
FT      TRANSMEM 170 186
FT      DOMAIN 187 327
FT      REPEAT 43 79
FT      REPEAT 80 123
FT      REPEAT 124 162
FT      DOMAIN 222 306
FT      DISULFID 44 55
FT      DISULFID 56 69
FT      DISULFID 78

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CC IsoId=Q93038-1; Sequence=Displayed;
 CC Name=2; Synonyms=LARD-1B;
 CC IsoId=Q93038-2; Sequence=VSP_006504;
 CC Name=3; Synonyms=WSL-S1, LARD-3;
 CC IsoId=Q93038-3; Sequence=VSP_006497, VSP_006498;
 CC Name=4; Synonyms=WSL-S2, LARD-2;
 CC IsoId=Q93038-4; Sequence=VSP_006501, VSP_006502;
 CC Name=5; Synonyms=LARD-4, LARD-11;
 CC IsoId=Q93038-5; Sequence=VSP_006495;
 CC Name=6; Synonyms=LARD-5;
 CC IsoId=Q93038-6; Sequence=VSP_006491, VSP_006495;
 CC Name=7; Synonyms=LARD-6;
 CC IsoId=Q93038-7; Sequence=VSP_006491, VSP_006494;
 CC Name=8; Synonyms=LARD-7;
 CC IsoId=Q93038-8; Sequence=VSP_006492;
 CC Name=9; Synonyms=LARD-8;
 CC IsoId=Q93038-9; Sequence=VSP_006491;
 CC Name=10; Synonyms=LARD-9;
 CC IsoId=Q93038-10; Sequence=VSP_006503;
 CC Name=11; Synonyms=Beta;
 CC IsoId=Q93038-11; Sequence=VSP_006496;
 CC Name=12; Synonyms=Beta soluble;
 CC IsoId=Q93038-12; Sequence=VSP_006499, VSP_006500;
 CC TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
 CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
 CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
 CC -1- SIMILARITY: Contains 4 TNR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
 CC residue instead of arginine.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y09392; CAA70561.1; -
 DR EMBL: Y09392; CAA70559.1; -
 DR EMBL: Y09392; CAA70560.1; -
 DR EMBL: Y07263; AAC50819.1; -
 DR EMBL: U83599; AAB41434.1; -
 DR EMBL: U83600; AAB41435.1; -
 DR EMBL: U78029; AAB40918.1; -
 DR EMBL: U74611; AAB39714.1; -
 DR EMBL: U94501; AAC51306.1; -
 DR EMBL: U94504; AAC51309.1; -
 DR EMBL: U94502; AAC51307.1; -
 DR EMBL: U94503; AAC51308.1; -
 DR EMBL: U94505; AAC51310.1; -
 DR EMBL: U94506; AAC51311.1; -
 DR EMBL: U94507; AAC51312.1; -
 DR EMBL: U94508; AAC51313.1; -
 DR EMBL: U94509; AAC51314.1; -
 DR EMBL: U94510; AAC51315.1; -
 DR EMBL: U94512; AAC51316.1; -
 DR EMBL: U83598; AAB41433.1; -
 DR EMBL: AF026070; AAC39356.1; -
 DR EMBL: AF026071; AAB82288.1; -
 DR EMBL: AB051850; BAB40662.1; -
 DR EMBL: AB051851; BAB40663.1; -
 DR EMBL: U75380; AAC51192.1; -
 DR EMBL: U75381; AAC51193.1; -
 DR EMBL: U83597; AAB41432.1; -
 DR Genew: HGNC:11910; TNFRSF25.
 DR MIM: 603366; -
 DR GO: GO:0005829; C:cytosol; NAS.
 DR GO: GO:0005887; C:integral to plasma membrane; TAS.
 DR GO: GO:0016329; F:apoptosis regulator activity; NAS.
 DR GO: GO:0005027; F:NGF/TNF (6 C-domain) receptor activity; TAS.

DR GO: GO:0004872; F:receptor activity; NAS.
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu...; TAS.
 DR GO: GO:0008624; P:induction of apoptosis by extracellular sig...; TAS.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_C6; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR Repeat: Apoptosis; Transmembrane; Alternative splicing; Signal;
 DR Repeat: Polymorphism.
 FT SIGNAL 1 24
 FT CHAIN 25 417
 FT DOMAIN 25 199
 FT TRANSMEM 200 220
 FT DOMAIN 221 417
 FT REPEAT 34 71
 FT REPEAT 72 115
 FT REPEAT 116 163
 FT REPEAT 164 192
 FT DOMAIN 332 413
 FT DISULFID 35 47
 Query Match 8.8%; Score 191; DB 1; Length 417;
 Best Local Similarity 22.9%; Pred. No. 5,1e-07;
 Matches 84; Conservative 46; Mismatches 153; Indels 82; Gaps 16;
 QY 81 CPFGHISE-----DGRDCISKYGOD---YSTHWNDDFLCLRTCD--SGEVELSP 128
 DB 51 CPAGHYLKAPCTERPCGNSCTGLVCP--QDFLAWENHNHS--ECARQACDEQASVALEN 106
 QY 129 CTTNRNVCCCEESTFE-----ESPCKRC-----RFGCRGAKVGDCT 171
 DB 107 CSAVADTRCCCKFEWFECQVSSQVSSPPYCCPCLDGLAHLHRTLLCSRRPTDGTCL 166
 QY 172 PW-----SDIECVHKSSG-----IIIGYVAANVLIVAVFCKSLMKK 210
 DB 167 PGFEHGDGCVSCTSLGSCPERCAVCGMRQFMWQVLAVGLVPLLLGATLLTYRRH 226
 QY 211 VLPYLGICSGGGGPERVDRSSORCGADNVNLNLSILQPTQVPEQMEVO-----E 264
 DB 227 CWPBKPLVTADDEAG---MEALTPPATHTLSPDASATTLAPDSSSEKICTVQLVGNSWT 282
 QY 265 PAEPYGNMLSPGS-----EHLLEPAEBSQRRLLVANEDPTTLR---QCFD 314
 DB 283 PGYPTQDALCPQVYWSMDQLPSRALGPAAP-----TISPESDAGSPAMILQPGPOLY 336
 QY 315 DFADLVFDSMEPLMRKLGIMDNEIKVAKAEAGHRTLYTMLIKWNKTRGDSVHTLL 374
 DB 337 DVMADVARRRKRKEVRLGLREAEIENVEVIGRFRQOYEMLKRW--RQOFRAGLGAVY 394
 QY 375 DAETLIG 381
 DB 395 AALERMG 401
 RESULT 12
 TNR6_HUMAN STANDARD; PRT; 335 AA.
 AC P24445; Q14292; Q14293; Q14294; Q14295; Q16652;
 DT 01-MAY-1992 (Ref. 22, Created)
 DT 01-MAY-1992 (Ref. 22, Last sequence update)
 DT 15-SEP-2003 (Ref. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS OR FASL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE-91309137; PubMed-1713127;
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RT Samehima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis.";
RL Cell 66:233-243(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 226-240; 269-291 AND
RP 321-335.
RX MEDLINE-92268122; PubMed-1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Poustngl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen.";
RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 6), AND FUNCTION.
RX MEDLINE-95181785; PubMed-7533181;
RA Cascino I., Flucci G., Papoff G., Ruberti G.;
RT "Three functional soluble forms of the human apoptosis-inducing Fas
RT molecule are produced by alternative splicing.";
RL J. Immunol. 154:2706-2713(1995).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RC TISSUE-Peripheral blood lymphocytes;
RA Schetzlein C.E., Poehlmann R., Philippson P., Eibel H.;
RN Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 4 AND 5).
RX MEDLINE-96238926; PubMed-8648105;
RA Papoff G., Cascino I., Eramo A., Starace G., Lynch D.H., Ruberti G.;
RT "An N-terminal domain shared by Fas/Apo-1 (CD95) soluble variants
RT prevents cell death in vitro.";
RL J. Immunol. 156:4622-4630(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE-Urinary bladder;
RX MEDLINE-22388257; PubMed-12477932;
RA Klausberg R.L., Feinhold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Keltman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP INTERACTION WITH RIPK1.
RX MEDLINE-95277838; PubMed-7538908;
RA Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
RT "RIP, a novel protein containing a death domain that interacts with
RT Fas/Apo-1 (CD95) in yeast and causes cell death.";
RL Cell 81:513-523(1995).
RN [8]
RP STRUCTURE BY NMR OF 218-335.
RX MEDLINE-97122332; PubMed-8967952;
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL Nature 384:638-641(1996).
RN [9]
RP VARIANT ALPS PRO-241.
RX MEDLINE-95300225; PubMed-7540117;
RA Fisher G.H., Rosenberg F.J., Straus S.E., Dale J.K., Middleton L.A.,
RA Lin A.Y., Strober W., Lenardo M.J., Puck J.M.;
RT "Dominant interfering Fas gene mutations impair apoptosis in a human
RT autoimmune lymphoproliferative syndrome.";
RL Cell 81:935-946(1995).
RN [10]
RP VARIANT ALPS TYR-260.
RX MEDLINE-97068823; PubMed-8929361;
RA Drappa J., Vaisnaw A.K., Sullivan K.E., Chu J.-L., Elkon K.B.;
RT "Fas gene mutations in the Canale-Smith syndrome, an inherited
RT lymphoproliferative disorder associated with autoimmunity.";
RL New Engl. J. Med. 335:1643-1649(1996).
RN [11]
RP VARIANT ALPS TRP-121 AND CYS-232.
RX MEDLINE-97180145; PubMed-9028321;
RA Bettinardi A., Brugnoni D., Quiros-Roldan E., Malagoli A.,
RA LaGutta S., Correria A., Notarangelo L.D.;
RT "Missense mutations in the Fas gene resulting in autoimmune
RT lymphoproliferative syndrome: a molecular and immunological
RT analysis.";
RL Blood 89:902-909(1997).
RN [12]
RP VARIANT ALPS ASP-257 AND SER-310.
RX MEDLINE-97180739; PubMed-9028957;
RA Sneller M.C., Wang J., Dale J.K., Strober W., Middleton L.A., Choi Y.,
RA Fleisher T.A., Lim M.S., Jaffe E.S., Puck J.M., Lenardo M.J.,
RA Straus S.E.;
RT "Clincial, immunologic, and genetic features of an autoimmune
RT lymphoproliferative syndrome associated with abnormal lymphocyte
RT apoptosis.";
RL Blood 89:1341-1348(1997).
RN [13]
RP VARIANT ALPS ALA-28.
RX MEDLINE-97463833; PubMed-9322534;
RA Pensati L., Costanzo A., Ianni A., Accapezzato D., Iorio R.,
RA Natoli G., Nisini R., Almerighi C., Balsano C., Vajro P., Vegnente A.,
RA Leyro M.;
RT "Fas/Apo1 mutations and autoimmune lymphoproliferative syndrome in a
RT patient with type 2 autoimmune hepatitis.";
RL Gastroenterology 113:1384-1389(1997).
RN [14]
RP VARIANT ALPS VAL-260.
RX MEDLINE-99038860; PubMed-9821419;
RA Infante A.J., Britton H.A., Denepoli T., Middleton L.A., Lenardo M.J.,
RA Jackson C.E., Wang J., Fleisher T., Straus S.E., Puck J.M.;
RT "The clinical spectrum in a large kindred with autoimmune
RT lymphoproliferative syndrome caused by a Fas mutation that impairs
RT lymphocyte apoptosis.";
RL J. Pediatr. 133:629-633(1998).
RN [15]
RP VARIANT ALPS LYS-241 AND GLN-250.
RX MEDLINE-99192346; PubMed-10090885;
RA Jackson C.E., Fischer R.E., Hsu A.P., Anderson S.M., Choi Y., Wang J.,
RA Dale J.K., Fleisher T.A., Middleton L.A., Sneller M.C., Lenardo M.J.,
RA Straus S.E., Puck J.M.;
RT "Autoimmune lymphoproliferative syndrome with defective Fas: genotype
RT influences penetrance.";
RL Am. J. Hum. Genet. 64:1002-1014(1999).
RN [16]
RP VARIANT ALPS GLY-272.
RX MEDLINE-99270228; PubMed-10340403;
RA Peters A.M., Kohlfink B., Martin H., Griesinger F., Wormann B.,
RA Gahr M., Roessler J.;
RT "Defective apoptosis due to a point mutation in the death domain of
RT CD95 associated with autoimmune lymphoproliferative syndrome, T-cell
RT lymphoma, and Hodgkin's disease.";
RL Exp. Hematol. 27:868-874(1999).
RN [17]

RP VARIANTS ALPS ARG-82; PRO-250; GLY-260 AND ILE-270.
 RX MEDLINE-99126461; PubMed-9927496;
 RA Vishnaw A.K., Orlicki J.R., Chu J.-L., Krammer P.H., Chao M.V.,
 RA Elkon K.B.;
 RT "The molecular basis for apoptotic defects in patients with CD95
 RT (Fas/Apo-1) mutations.";
 RL J. Clin. Invest. 103:355-363(1999).
 RN [18]
 RP VARIANTS NON-HODGKIN'S LYMPHOMA THR-25; PHE-180; LEU-183; ILE-198;
 RP VAL-260; LYS-264; LYS-272; PHE-278 AND ASN-299.
 RX MEDLINE-99003325; PubMed-9787134;
 RA Groenbaek K., Straten P.T., Ralikiær E., Ahrenkiel V., Andersen M.K.,
 RA Hansen N.E., Zeuthen J., Hou-Jensen K., Guldberg P.;
 RT "Somatic Fas mutations in non-Hodgkin's lymphoma: association with
 RT extranodal disease and autoimmunity.";
 RL Blood 92:3018-3024(1998).
 RN [19]
 RP VARIANTS ALPS PRO-241; VAL-260; ILE-270 AND GLY-272.
 RX MEDLINE-21311411; PubMed-11418480;
 RA Straus S.E., Jaffe E.S., Puck J.M., Dale J.K., Elkon K.B.,
 RA Roosen-Wolff A., Peters A.M.J., Sneller M.C., Hallahan C.W., Wang J.,
 RA Fischer R.E., Jackson C.M., Lin A.Y., Baemler C., Siegfert E.,
 RA Marx A., Vishnaw A.K., Grodzicky T., Fleisher T.A., Leonardo M.J.;
 RT "The development of lymphomas in families with autoimmune
 RT lymphoproliferative syndrome with germline Fas mutations and
 RT defective lymphocyte apoptosis.";
 RL Blood 98:194-200(2001).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both. The secreted isoforms 2 to 6 block apoptosis (in vitro).
 CC -1- SUBUNIT: Binds DAXX (by similarity). Binds RIPK1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
 CC Secreted (isoforms 2 to 6).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC
 Query Match 8.7%; Score 189; DB 1; Length 335;
 Best Local Similarity 22.1%; Pred. No. 5.5e-07;
 Matches 85; Conservative 63; Mismatches 131; Indels 106; Gaps 16;
 38 LVLVVAVLLV---VSAESALITQODLAPQRAAPQKKSSPESEGL-----CPR 83
 8 LPLVLTVSARLSSKSVNAQVTDINSKGL--ELKRTVTTFETQNLGHHGQFCFKPCPP 65
 84 GHH-----ISEDGRDCISCKYGGDYSTHNNDLFLCRTCRODSG---EVELSPCTTTRN 134
 66 GERKARDCYVNGDEPPCVPEQGEKEYTDKAHFSKSKRCRLCDGSHLEVEIN--CTTQN 124
 135 TVOCCEGTREDSPMKCKKRTGCGRGWKKYGDCTPMSDIECVHKEGIIIGVAAV 194
 125 TKCRCKNFPCNSVTCEHCDCPC--TKCEHGIK--ECTLTSNTKCKEKGSSNLG----- 175
 195 VLIYAIVVCKSLMKKLYPLTKIGICSGGGDPERVYDSSORPGADVNLMEIYSIILOPTQ 254
 176 -----WCLLLLPILITVWVK-----RKQVQTKRKHREKNGSHS-----SPTL 215
 255 VPQEQMEVQPAEFTGVNMLSPGESEHLTPAEAEKRSQRRLLYPANEGDPTETLRQCFD 314
 216 NP-----ETVALNLSVDVLSKYI-----T 234
 315 DFADLYVPFDSWEPMLKRLGLMDNEIKYAKAAAGHRDYL---YMLIKWVNTKGRDASVH 371
 235 TIAGVMTLSOVKGVKRNKV--NEAKIDEIKNDNVQDAOKVOLLRNHMLHGKREAYD 292
 372 TILDALD-----TLGERLAKOKIED 391
 293 TLIKDKKANLCTLAETIOTIILKD 317

RESULT 13
 ID TNR6_BOVIN STANDARD; PRT; 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
 DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen)
 DE (CD95).
 GN TNFSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96226401; PubMed-8634151;
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.";
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
 CC recruits caspase-8 to the activated receptor. The resulting death-
 CC inducing signaling complex (DISC) performs caspase-8 proteolytic
 CC activation which initiates the subsequent cascade of caspases
 CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
 CC mediated apoptosis may have a role in the induction of peripheral
 CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
 CC both (by similarity).
 CC -1- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
 CC -1- SIMILARITY: Contains 1 death domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U34794; AAC48546.1; -;
 DR HSSP; P25445; IDDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00531; death; 1.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;
 FT SIGNAL 1
 FT CHAIN 17 323
 FT
 FT DOMAIN 17 170
 FT SUPERFAMILY MEMBER 6.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 171 188
 FT TRANSMEM 189 323
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT DOMAIN 238 306
 FT DISULFID 45 56
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 FT DISULFID 79 82
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FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
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FT DISULFID 182 195 BY SIMILARITY.
FT DISULFID 185 191 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
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DA/BKL AND F344/NHSD).
FT VARIANT 295 295 H -> P (IN STRAINS LEW/NHSD, ACI/SEGHSD,
DA/BKL, F344/NHSD AND BV/SSNHSD).
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Best Local Similarity 21.6%; Pred. No 8.3e-06;
Matches 104; Conservative 58; Mismatches 153; Indels 167; Gaps 25;

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OY 30 PGLRVPKTLVVAAYALLV--SAESALI-TQODLAPQORAPQOKRSPSEG----LC 81
DB 7 PGL-----LSTLVLLALMLGHPGVTLGVLPSLDREKRDNLCPQGXAHKNNISICTKC 62
OY 82 PRGHHSIED-----GRD--CISCXYGDDYSTRHNDLFLCLACTRC--DSGEVELSPCTTTR 133
DB 63 HKGTLYVSDCPSPGQETVCEVCDKG--TFETASQNHVROCLSCKCRKEMFQVEISPCRAM 121
OY 134 NTWCOCCEGTFRF--EDSPFMRCKRCRTGCPRGWKV-----GDCY 171
DB 122 DTVCCKKNOFQRYLSTHFCQVDC--SPCNGTYTIPCKEKQNTVCNCHAGFLSGNECT 180
OY 172 PMS---DIECVH-----KESGIIIGVTAAYV-LIYAVFVCKSL-----WK 209
DB 181 PCSHCKKNQCKMLCLPVAANTNPQDSGAVALLPLVIFLGLCLFETICISILCRYQW- 239
OY 210 KVLPLYLKGICGGGGERVDRSSQRPAGADNVLNEIVSTLQPYVPEQME-----VQEP 265
DB 240 -----RP-----RVYSIICRDSAPVKEVEGEGIVTKP 266
OY 266 AEPTGVNMLSPGE-----SEHLLEPAERSQRR-----RLVAPANE 302
DB 267 LTPASIPAFSPNGFNPTLCFSTTPRSHVSSPTIPSPVFGPSWNMFVPPVREVPYQG 326
OY 303 GDP-----TEFLRQCFDDFA-----DLVPFDSWEPLMRKLG 333
DB 327 ADPLLYGSLNPVPIPAVFKMEDVVAAPQRLDTADPAMLYAVYDGVPTRWKEFNRLG 386
OY 334 LMDNET-KVAKAEAGHDTLTMLIKWVKTKG-----DASYHTLID-----ALEPLGE 382
DB 387 LSHETIERELQNGRCLEAHYSMLEAMRRRTPRHEATLIDVGRVLCDMNLRGCLENIRE 446
OY 383 RL 384
DB 447 TL 448
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Search completed: August 4, 2003, 15:17:55
Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:14:55 ; Search time 42 Seconds

(without alignments)
941.079 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169

Sequence: 1 MEORCONAPASGARRKHP.....HLTSGKMYLEGNADSAXS 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238.5	11.0	461	2 JC4302	tumor necrosis fac
2	210.5	9.7	455	1 GOMST1	tumor necrosis fac
3	209	9.6	454	1 GOMST1	tumor necrosis fac
4	192	8.9	327	2 A46484	apoptosis-mediati
5	189	8.7	335	2 A40036	tumor necrosis fac
6	179	8.3	435	2 I54182	tumor necrosis fac
7	175.5	8.1	461	1 GORT1	tumor necrosis fac
8	173.5	8.0	314	2 I37383	FAS soluble protei
9	158	7.3	324	2 JC2385	Fas antigen precu
10	152	7.0	416	1 JN0006	nerve growth facto
11	151.5	7.0	461	1 A35356	tumor necrosis fac
12	142.5	6.6	425	1 A26431	nerve growth facto
13	142.5	6.6	427	1 GOMST1	hypothetical prote
14	141.5	6.5	348	2 T28623	gene murine tumou
15	139	6.4	459	2 I48854	gene G4R protein - vari
16	138.5	6.4	349	2 D72175	gene G4R protein - vari
17	138.5	6.4	349	2 D36858	gene G4R protein - vari
18	135	6.2	474	2 B38634	gene G4R protein - vari
19	133.5	6.2	271	2 SI2783	OX40 antigen precu
20	131.5	6.1	272	2 I48700	gene OX40 protein
21	130	6.0	272	2 A60771	B-cell activation
22	122	5.6	326	1 GOMST1	T2 protein - myxom
23	122	5.6	595	2 A42086	CD30 antigen precu
24	120	5.5	1372	2 T25933	hypothetical prote
25	118.5	5.5	1036	2 T17405	scavenger receptor
26	117	5.4	277	2 I37552	OX40 homolog - hum
27	114.5	5.3	651	2 JC7705	death receptor - hum
28	114	5.3	305	2 A46476	B cell-associated
29	113.5	5.2	256	2 B32393	T-cell antigen 4-1

30	113.5	5.2	1356	2 A45445	janusin precursor,
31	112.5	5.2	557	2 A48434	variant-specific s
32	112	5.2	1353	1 JH0675	restictin precurs
33	111.5	5.1	1810	1 A32230	tenascin precursor
34	110.5	5.1	962	2 JC5571	subtilisin-like pr
35	110.5	5.1	975	2 JC5570	subtilisin-like pr
36	110.5	5.1	1548	2 S34583	serine proteinase
37	110	5.1	325	2 B43692	T2 protein - rabbi
38	108.5	5.0	913	1 A47543	R-cadherin precurs
39	108	5.0	1346	2 A57376	probable regulator
40	108	5.0	2824	2 T22759	hypothetical prote
41	107.5	5.0	327	2 T01038	myb-related protei
42	107.5	5.0	905	2 S55059	fertilin alpha-1 -
43	106.5	4.9	291	2 S42075	beta-lactamase (EC
44	106.5	4.9	2201	2 A32160	tenascin-C - human
45	106	4.9	398	1 S24802	polyferredoxin 6x2

ALIGNMENTS

RESULT 1	
JC4302	tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)	
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 23-Jul-1999	
C:Accession: JC4302; PC4093	
R:Suter, B.; Pauli, U	
Gene 163, 263-266, 1995	
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.	
A:Reference number: JC4302; MUID:96011645; PMID:7590278	
A:Accession: JC4302	
A:Molecule type: mRNA	
A:Residues: 1-461 <SUT>	
A:Cross-references: GB:019994; NID:91141752; PIDN:AAC48499.1; PID:91141753	
A:Accession: PC4093	
A:Molecule type: protein	
A:Residues: 1-7 <SUT>	
A:Experimental source: kidney cell line 15	
C:Genetics:	
A:Gene: Unif	
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology	
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor	
F:1-29/Domain: signal sequence #status predicted <SIG>	
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>	
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>	
F:44-82/Domain: NGF receptor repeat homology <NGF>	
F:211-231/Domain: transmembrane #status predicted <TM>	
F:361-447/Domain: signal transduction #status predicted <ST>	
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted	
Query Match	11.0%, Score 238.5; DB 2; Length 461;
Best/Local Similarity	24.4%; Pred. No. 8.5e-10;
Matches 117; Conservative 58; Mismatches 164; Indels 141; Gaps 26;	
OY	30 PGLVPRKTVLVVAAYLVLLV---SAESALLITQOOLAPQGRAPQGRKSPSE-----GLC 81
DB	7 FGLLP-----LVRLALVDVYRAGVHGLVLRPGDEKRESLCPOGKYSHPNRSITCTK 62
OY	82 PGRHSHSD-----GRDCISCKYGOQDYSTMNDLFCIRCTKSDS--GEVELSPCTTTR 133
DB	63 HKGTLYLHNDCLGPGIDTCRECDNG-FTTASBNHLTQCLSSKRSMSQYIEISCTYDR 121
OY	134 NTVQCQCEEGTFRSDSPM--CRKCRGCGPRGMKVGSDCTPWSDIETVHKESGIIII---- 187
DB	122 DTVCGCRKNQYRKYSSETLFOCLNCSTL-CPNGFVQL-PCLEKQPTIC-NCHSGFELRDK 178
OY	188 -----GTVAAVYI-----VAIV-----CKSLW 208
DB	179 CVSCVNCNKADCKNLCPATSETRNDPDTGTVLLPLVIFFGCLAFELVGLACRYQRW 238
OY	209 KKVLPYKLGICSGG-----GDPERVDRS-----SORPGAEDVNLIEIVSIL 250

Db 239 K---PKLYSIICGKSTPVKEPEPLATAPSFCDITTFSPSPSPPTTFSPSPSPIS 295
251 QPTQVPE--EDMEKQEEPAE-----PTGVNMLSP-----GSEHLLERPEA 288
Db 296 SPFTTCDMSNIKTSPKRIAPPQAGPILPMPAPSTVPYPLPKWGGSAHSAHSA 355
QY 289 ERSQRRLILVPAWGDPTETLRQCFADLVFPDSNEPLRLKGLMDNEI-KYAKAEAA 347
Db 356 QLA-----DADA-TLYAVVDG---VPTPRKKEFRRLGSEHELERLELNGR 400
QY 348 GHRDTLYTMLIKVKNKGG-RDASVH-----TLDAETLGERL---AKQIEDHL 394
Db 401 CLREAQYMLAEWRRRTSRREATLELLGSLVLRDMLLGLCEDIEALRGARLAPAPHL 460

RESULT 2
GQHQUT1
tumor necrosis factor receptor 1 precursor [validated] - human
N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1
N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
C:Accession: A38208; A34899; A34900; A36555; A38281; S12057; J70758; A60231; A38
R:Funcs: P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.
A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization to ch
A:Reference number: A38208; MUID:92250049; PMID:1315717
A:Accession: A38208
A:Molecule type: DNA
A:Residues: 1-455 <FUC>
A:Cross-references: GB:M75864; GB:M75865; GB:M75866; NID:9339748; PIDN:AAA61201.1; PID:G
R:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tachibana, H.; Lessl
Cell 61, 351-359, 1990
A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep
A:Reference number: A34899; MUID:90235284; PMID:2158862
A:Accession: A34899
A:Molecule type: mRNA
A:Residues: 1-455 <LOE>
A:Cross-references: GB:M58286; GB:M3480; NID:9339753; PIDN:AAA6753.1; PID:9339754
A:Experimental source: Placenta
A:Note: Part of this sequence, including the amino end of the mature protein, confirmed
R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Galanaga, T.
Cell 61, 361-370, 1990
A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor
A:Reference number: A34900; MUID:90235285; PMID:2158863
A:Accession: A34900
A:Molecule type: mRNA
A:Residues: 1-455 <SCH>
A:Cross-references: GB:M33294; NID:9339744; PIDN:AAA03210.1; PID:9339745
R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recept
A:Reference number: A36555; MUID:91090841; PMID:1702293
A:Accession: A36555
A:Molecule type: mRNA
A:Residues: 1-455 <HTM>
A:Cross-references: GB:M63121; NID:9339755; PIDN:AAA6754.1; PID:9339756
A:Accession: C36555
A:Molecule type: protein
A:Residues: 30-361-41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104, 107-128, 162-167, 'X', 169-2
A:Note: The purified protein, called tumor necrosis factor binding protein, is a soluble
R:Gay, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re
A:Reference number: A38281; MUID:91017509; PMID:2170974
A:Accession: A38281
A:Molecule type: mRNA
A:Residues: 1-455 <GRA>
A:Cross-references: GB:M37764
R:Koppar, Y.; Kemper, O.; Brakelbusch, C.; Engelmann, H.; Zwarg, R.; Adierka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990

A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the
le form of the receptor.
A:Reference number: S12057; MUID:91006021; PMID:1698610
A:Accession: S12057
A:Molecule type: mRNA
A:Residues: 1-455 <NDP>
A:Cross-references: EMBL:X55313; NID:937223; PIDN:CAA39021.1; PID:937224
A:Note: Parts of soluble TNF binding protein 1, including its amino and carboxyl ends
R:Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A:Title: Cloning and partial characterization of the promoter for the human p55 tumor
A:Reference number: J70758; MUID:94085779; PMID:8262379
A:Accession: J70758
A:Molecule type: DNA
A:Residues: 1-13 <KEM>
R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequ
A:Reference number: A60231; MUID:90292116; PMID:2113477
A:Accession: A60231
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'X', 55-57 <SEC>
R:Galanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Luccl III, J.A.; Jeffes, E.W.B.;
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa
lients.
A:Reference number: A38258; MUID:91062364; PMID:2174164
A:Accession: A38258
A:Molecule type: protein
A:Residues: 41-60 <GAT>
A:Experimental source: cancer patient serum
R:Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyrell, H.; Grubb, A.; Adolf, G.
Eur. J. Haematol. 42, 270-275, 1999
A:Title: Isolation and characterization of a tumor necrosis factor binding protein fr
A:Reference number: A60594; MUID:89171156; PMID:2924890
A:Accession: A60594
A:Molecule type: protein
A:Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 <OLS>
A:Experimental source: renal failure patient urine
R:Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Eviden
A:Reference number: A35010; MUID:90110215; PMID:2153136
A:Accession: A35010
A:Molecule type: protein
A:Residues: 41-45 <ENG>
A:Experimental source: normal urine
R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A:Reference number: JC2404; MUID:95128033; PMID:7765720
A:Accession: JC2404
A:Molecule type: protein
A:Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>
A:Experimental source: urine
A:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
C:Genetics:
A:Gene: GDB:TNFR1
A:Cross-references: GDB:125913; OMIM:191190
A:Map position: 12p13.2-12p13.2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Domain: signal sequence #status predicted <SIG>
F:30-211/Domain: extracellular #status predicted <EXT>
F:41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #stat
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:137-167/Domain: NGF receptor repeat homology <NG3>
F:168-196/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-455/Domain: intracellular #status predicted <INT>

RESULT 6

tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.

Genomics 16, 214-218, 1993

A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequences

A:Reference number: I54182; MUID:93252381; PMID:8486360

A:Accession: I54182

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-435 <RES>

A:Cross-references: GB:I04270; NID:9339761; PIDN:AAA36757.1; PID:9339762

C:Genetics:

A:Gene: GDB:LTBR

A:Cross-references: GDB:1230195; OMIM:600979

A:Map position: 12p13.3-12p13.1

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match

Best Local Similarity 8.3%; Score 179; DB 2; Length 435;

Matches 72; Conservative 28; Mismatches 91; Indels 100; Gaps 15;

QY 81 CRRGHHSDD---RD--CISCKYGDYSTHNNDLFLCRLCTRC--DSEVELSPCTTR 133

DB 62 CRRGHHSDD---RD--CISCKYGDYSTHNNDLFLCRLCTRC--DSEVELSPCTTR 120

QY 134 NTVCOCSESTFRE-----EDSP-----EMCRKCRGTG----- 159

DB 121 KQCGCQCPREMFCAAMALECTHELSDCPRTGAEALKDEYKGNHNVCKKAGHQNNTSS 180

QY 160 -----CP-RGNKVVGDCTPMSDIECVH-----KESGIIIGVTY---AAVLI 197

DB 181 PSARCOPHTRCENOGILEAPGTASDTTCKNPLLEPRMGGTMIAMLVLLPLAFLLD 240

QY 198 VAVFVCKSLKMK-----KVLRYLKIGICSGGGGDEPERYDRSSQRCAGADVNLNEVSL 250

DB 241 ATTFVSC---IMKSHPSLCKLGLSLRRPQSGSPNV---AGSWERPKNHYPFDLQPL 294

QY 251 OPTQ-----VPEQEMVEQEPAPRTGVNMLSPGSEHL 282

DB 295 LPISGDVSPVSTGLPAAPVLEAGVPPQ-----QSPDLDTREPLEPDEQSQV 341

Db 295 LPISGDVSPVSTGLPAAPVLEAGVPPQ-----QSPDLDTREPLEPDEQSQV 341

RESULT 7

tumor necrosis factor receptor 1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999C:Accession: B36555
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantze, M.;DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor

A:Reference number: A36555; MUID:91090841; PMID:1702293

A:Accession: B36555

A:Molecule type: mRNA

A:Residues: 1-461 <HIM>

A:Cross-references: GB:M63122; NID:9207361; PIDN:AAA42256.1; PID:9207362

C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>

F:30-211/Domain: extracellular #status predicted <EXT>

F:30-201/Product: tumor necrosis factor binding protein #status predicted <BTP>

F:44-82/Domain: NGF receptor repeat homology <NG1>

F:84-126/Domain: NGF receptor repeat homology <NG2>

F:127-167/Domain: NGF receptor repeat homology <NG3>

F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MTM>
F:235-461/Domain: intracellular #status predicted <INT>
F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 8.1%; Score 175.5; DB 1; Length 461;

Matches 104; Conservative 58; Mismatches 153; Indels 167; Gaps 25;

QY 30 PCLRPKTLVVAVALLV---SASALI-TQODLAPQGRAPQGRKSSPSG-----LC 81

DB 7 PCL---LTLVLALMLGTHPSGVTLVPSLGRKRNLCPCQGYAHPKNNSICCTKC 62

QY 82 PRGHHSDD---GRD--CISCKYGDYSTHNNDLFLCRLCTRC--DSEVELSPCTTR 133

DB 63 HKGYLVSDCPSRPGQETVEYCDKG-TFTASQNHVRQCLSKCTCKREMGVLEISCKAM 121

QY 134 NTVCOCSESTFRE-----EDSPKCRKCRGTGCPGMKV-----GDCT 171

DB 122 DTVCGCKKNQFORVLETHFQCVDC-SPCFNGTVTIPCKEKONTVCNCHAGFFLSGNET 180

QY 172 PMS---DIECVH-----KESGIIIGVTYAAVY-LIVAVFVCKSL-----WK 209

DB 181 PSCHCKKNQCKMLCLPVAANTNPQDSTAVLLPLVIFLGCLLFFICTISLCRYQW- 239

QY 210 KVLRYLKIGICSGGGGDEPERYDRSSQRCAGADVNLNEVSLLOPTQVPEQEME-----VQBP 265

DB 240 -----RP-----RVYIILCRDSAPKVEGEGVITKP 266

QY 266 AEPGVNMLSPG-----SEHLEPAEARSOR-----RLVPAVE 302

DB 267 LTPASIPAPSPNGFNPGLTFSTPRFSHPVSTPISPVFGSPNMHNPVPRVPPQSG 326

QY 303 GPP-----TETLQCCFDPA-----DLVPDSMEPLMRKG 333

DB 327 ADPLVGLSNPVPVIRAPVARKMEDVVAAPQRLDTADPAMLVAVVQGVPRPKRKEFRLLG 386

QY 334 LMDNEI-KVAKAEAGHRTLYTLIKVNTKGR-----DASVHTLLD-----ALETLGE 382

DB 387 LSEHETERLELNGRCLREAHNSMLEAMRRRTPRHATIDVVGRYLCDNNLGCLEINIE 446

QY 383 RL 384

DB 447 TL 448

RESULT 8

FAS soluble protein - human

C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000C:Accession: I37383
R:Casano, I.; Ficuci, G.; Papoff, G.; Rubertl, G.J. Immunol. 154, 2706-2713, 1995
A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule

A:Reference number: I37383; MUID:95181785; PMID:7533181

A:Accession: I37383

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-314 <RES>

A:Cross-references: EMBL:Z47993; NID:9728578; PIDN:CAA88031.1; PID:9695539

Query Match

Best Local Similarity 8.0%; Score 173.5; DB 2; Length 314;

Matches 51; Conservative 25; Mismatches 59; Indels 29; Gaps 8;

QY 38 LVLVVAVALLV---VSASALITQODLAPQGRAPQGRKSSPSG-----CPP 83

DB 8 LPLVLTVARLSKSSVNAQVTDINSKGL--ELRKVTVTETQNLBGLHHDGQFCRHKPCP 65

QY 84 GHH-----ISDGRCISCKYGDYSTHNNDLFLCRLCTRDSG---EVELSPCTTYTN 134

DB 66 GERKARDCTVNGDEPDCVPCQSGKEVTDRAHSSKCRRLCDGGLVEIN-CTRQN 124

R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires, R. *Proc. Natl. Acad. Sci. U.S.A.* 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A:Reference number: A36475; MUID:91045991; PMID:2172983
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195; 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Demble, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
 Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A:Reference number: A48416; MUID:91370690; PMID:1966549
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA819824.1; PID:g235649
 A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A:Reference number: A36007; MUID:90349572; PMID:2166946
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AAA6362.1; PID:g339752
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
 J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A:Reference number: A23666; MUID:91056048; PMID:2173696
 A:Accession: A23666
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 23-40; 65-69; 136-141; 300-306 <LOE>
 R:Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:9010215; PMID:2153136
 A:Accession: A35010
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 27-31 <ENG>
 R:Kubnert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: I38094; MUID:95121934; PMID:7821811
 A:Accession: I38094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:9825701
 C:Genetics:
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:191191
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: the list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 151.5; DB 1; Length 461;
 Best Local Similarity 26.8%; Pred. No. 0.0018;

Matches 63; Conservative 19; Mismatches 86; Indels 67; Gaps 14;
 QY 81 CPPEHH-----ISDGRDLCISKGGDYSTRHMNDLFLCRLR-TCDSGGEVELSCTTTRN 134
 Db 57 CSPGQHNKVRCTKTSDFVDCSE--DSTYTDLMMNVBPCLSCSGSCSDQVETQACTREON 115
 QY 135 TVCCCEGTEFREEDSPENC-----RKCPRGCPGMVGDCTPWSIDIECVHKESGILLIG 188
 Db 116 RICRGRGWICALSKQEGCRCLAPLRRCRGF--GVARPG--TTSIDVYCKPCAPRGTFSN 171
 QY 189 VTVA-----VVLIVAV-----FVCSLKKKVLPLYKIGICSGGGGDPERYDRSSQ 234
 Db 172 TTSSTDICRPHQICNVVAIPGNASMDAVCTST-----SPTR-----SM 209
 QY 235 RPGAEDVNLNFIYSIILOTPVPRDME-VQPARPTGVNMLSP-GESEHLLPRAE 287
 Db 210 APGA-----VHLPPVSTRSQHTOPTPEPSTAPSTFLLPMPGS---PPAE 252
 RESULT 12
 A26431
 Nerve growth factor receptor precursor, low affinity - rat
 N:Alternate names: NGF receptor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 R:Radek, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
 Nature 325, 593-597, 1987
 A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
 A:Reference number: A26431; MUID:87115859; PMID:3027580
 A:Accession: A26431
 A:Molecule type: mRNA
 A:Residues: 1-425 <RAD>
 A:Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
 R:Metz, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
 Gene 121, 247-254, 1992
 A:Title: Regulatory elements and transcriptional regulation by testosterone and retin
 A:Reference number: PH1229; MUID:93077038; PMID:1446821
 A:Accession: PH1229
 A:Molecule type: DNA
 A:Residues: 1-20 <MET>
 A:Cross-references: GB:X61269
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all
 C:Comment: This protein is thought to form a high-affinity receptor when it associate
 C:Genetics:
 A:Introns: 20/3
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
 F:30-251/Domain: extracellular #status predicted <EXT>
 F:33-66/Domain: NGF receptor repeat homology <NG1>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-148/Domain: NGF receptor repeat homology <NG3>
 F:150-190/Domain: NGF receptor repeat homology <NG4>
 F:198-249/Region: serine/threonine-rich
 F:252-273/Domain: transmembrane #status predicted <TMN>
 F:274-425/Domain: intracellular #status predicted <INT>
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 142.5; DB 1; Length 425;
 Best Local Similarity 22.8%; Pred. No. 0.0075;
 Matches 87; Conservative 38; Mismatches 142; Indels 115; Gaps 16;

QY 71 QKRSSPSEGLCPGHHSIEDGRDLCISKY--QDYSTRHMNDLFLCRLRCDSEVELSP 128
 Db 94 QSMSAP-----VEADDVAV-RCAYGYQDEETG-----HCEACSVCEVSGSLVFS 138
 QY 129 CTTTRNRYC-QCEGCTFAEE-DSEPMKCKCTGCPRGWVKKGDDCTPMSDIC----- 178
 Db 139 CQDKQNTVCCECPGEGTYSDEANHVDPCLPC-TVCEDTERQRLRECTPMADACEIEIPGRW 197

OY 179 -----VKESGIIIVAAVLIVAVFCKSLMKVLPYLKGI 218
 Db 198 PRSTPEGSSTAPSTOPEPEBQDLVPS--TVADMVTTM----- 237
 OY 219 CSGGGCDEPERVDRSSQRGADNVLNLSILOPTQVP-----EQEMEVOEPAP 268
 Db 238 ----GSSOPVYTR-----GTTDNILPYVCSILAAVVLVAVIAEKRNNSCKONOGANS 288
 OY 269 TGVNMLSPGESEHIL-----LEPAEERSQRRLLVLPANEGDPT-----ETLRQCF 313
 Db 289 RPNVQTPPEGEKHLHSDGISVDSGLHDQOTHTQTASGQALKGNGNLXSLPLTKR--- 345
 OY 314 DDFADLVFPDSMEPLMKRLGLMDEIKYAKAPAGHRDTLYTMLIKWNKTGRDASVHTL 373
 Db 346 EEVEKLNGDYWRHLAGELGYOPEHIDSFTEHACFVR----ALLASW-----GAQDSAT 395
 OY 374 LDALETGERLAKOKIEDHLLS 395
 Db 396 LDALLALRRIQRADIVESLCS 417

RESULT 13

GOHUN

nerve growth factor receptor precursor, low affinity [validated] - human
 N:Alternate names: NGF receptor
 C:Species: Homo sapiens (man)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-2000
 C:Accession: A25218; A60204; S21689; I57638

R:Johnson, D.; Ianahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Botwell, M.
 Cell 47, 545-554, 1986

A:Title: Expression and structure of the human NGF receptor.
 A:Reference number: A25218; MUID:87051725; PMID:3022937

A:Accession: A25218

A:Molecule type: mRNA

A:Residues: 1-427 <JOB>

A:Cross-references: GB:M14764; NID:g189204; PIDN:AAA59544.1; PID:g189205

R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
 J. Neurochem. 48, 225-232, 1987

A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
 A:Reference number: A60204; MUID:87085574; PMID:3025363

A:Accession: A60204

A:Molecule type: protein

A:Residues: 29-31,'T',33-42,'T',45-46,'T',50-51,'X',54-56 <MAR>

A:Experimental source: melanoma cell line A875

A:Note: this sequence has been corrected by a note added in proof to follow the nucleotid
 R:Visavayaiah, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.

Arch. Biochem. Biophys. 294, 244-252, 1992

A:Title: Structural domains of the extracellular domain of human nerve growth factor rec
 A:Reference number: S21689; MUID:92198017; PMID:1372492

A:Accession: S21689

A:Status: preliminary

A:Molecule type: protein

A:Residues: 183-208 <VIS>

R:Sehgal, A.; Patil, N.; Chao, M.

Mol. Cell. Biol. 8, 3160-3167, 1988

A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
 A:Reference number: I57638; MUID:89096903; PMID:2850481

A:Accession: I57638

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-22 <RES>

A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
 C:Comment: The cytosolic-rich region of the extracellular domain may form part of all of
 C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:

A:Gene: GDB:NGFR

A:Cross-references: GDB:I20234; OMIM:162010
 A:Map position: 17q21-17q22
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
 F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-427/Product: nerve growth factor receptor #status experimental <MAR>
 F:29-250/Domain: extracellular #status predicted <EXT>
 F:32-65/Domain: NGF receptor repeat homology <NG1>
 F:67-108/Domain: NGF receptor repeat homology <NG2>
 F:109-147/Domain: NGF receptor repeat homology <NG3>
 F:149-189/Domain: NGF receptor repeat homology <NG4>
 F:197-248/Region: serine/threonine-rich
 F:251-272/Domain: transmembrane #status predicted <TRM>
 F:273-427/Domain: intracellular #status predicted <INT>
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.6%; Score 142.5; DB 1; Length 427;
 Best Local Similarity 20.0%; Pred. No. 0.0075;
 Matches 86; Conservative 44; Mismatches 143; Indels 157; Gaps 17;

OY 81 CPFGHITSEDRDSCIKYGDY-----SHNMDLF-----CLRCRCD 120
 Db 32 CPTGLY-THSEGCCACNLGCVAPCCGANOVCPCIDSVTSDDVVSATPECKPCTECV 90
 OY 121 SGEVELSPCTTTRNTVCCCEGTREEDSP--EMCRKCRG-----CP 161
 Db 91 GLQSMAPCVADADAVCAAYGYODETGTGCEACRCVCEASGLVFSQDQKNTVCECP 150
 OY 162 RGMV-----KVGDCTPMSDIECVH----- 180
 Db 151 DGTYSDEANHYDPLCTVCEDETERQLECRMADECEIPIGRWITRSTPEGSSTAP 210
 OY 181 -----KESGIIIGVVAANVLV-----AVFCKSLMKVLPYLKGI 218
 Db 211 STQEPAPPEODLASTVAGVTVTWGSSQPVTRGTTNLTIPYCSILAAVVLVAVI 270
 OY 219 C-----SCGGGDEPERVDRSSQRGADNVLNLSILOPTQVPEQEMEVOEPAE 267
 Db 271 AFKRNNSCKONOGANSR-----VNOTPEEGEKLHSDGL-----SVDSGLHDQPH 321
 OY 268 PT--GVNMLSPGESEHILPEAEERSQRRLLVPAANGDPETLRQCFDFADLVPPDSW 325
 Db 322 QTASGOALKGDDGYSSLPAPKREVER--LLNGSAG-----DTW 359
 OY 326 EPLRKILGMONEIKVAKAEAGHRDTLYTMLIKWNKTGRDASVHTLDALETGERLA 385
 Db 360 RHLGELCYOPEHIDSFTEHACFVR----ALLASW--TQDSATLDALLAL-----RRIQ 409
 OY 386 KQKIEDHLLS 395
 Db 410 RADIVESLCS 419

RESULT 14

T28623

hypothetical protein G2R - variola major virus
 C:Species: variola major virus

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T28623

R:Massung, R.F.; Esposito, J.J.; Liu, L.T.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au
 Nature 366, 748-751, 1993

A:Title: Potential virulence determinants in terminal regions of variola smallpox vir
 A:Reference number: Z20488; MUID:94088747; PMID:8264798

A:Accession: T28623

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-348 <MAS>

A:Cross-references: EMBL:I2579; NID:9623595; PIDN:AAA60933.1; PID:9439102

A:Experimental source: strain Bangladesh 1975

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 6.5%; Score 141.5; DB 2; Length 348;
 Best Local Similarity 29.4%; Pred. No. 0.0071;

Matches 42; Conservative 17; Mismatches 57; Indels 27; Gaps 8;

OY 53 SALTQODLAFQQAQQRSSPSEC-----LCPGCHHT-----SEDRGDCISCKY 99
 Db 13 SCIIINGDAAY--TPPNCCKDTEYKRHNHLCCLSCPPTGYSRLCDSTNTDCTPCGS 69

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 15:07:40 ; Search time 86 Seconds

(without alignments)
758.565 Million cell updates/sec

Title: US-10-052-798-1

Perfect score: 2169
Sequence: 1 MGRGQNPADPAGARRKRRP.....HLISGKFWYLRGNADSAKS 411

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_19Jun03:*

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2167	99.9	411	19	AAW79261
2	2167	99.9	411	20	AAW888410
3	2167	99.9	411	20	AAW83321
4	2167	99.9	411	21	AAW55805
5	2167	99.9	411	22	AAU04038
6	2167	99.9	411	22	AAW73442
7	2167	99.9	411	22	AAW73443
8	2167	99.9	411	23	ABG31490
9	2167	99.9	411	23	AAW51080

10	2167	99.9	411	23	AAU76947	Human Apo2 protein
11	2167	99.9	411	23	ABG09602	Amino acid sequenc
12	2167	99.9	411	24	ABG75645	Human Tango-63e pr
13	2167	99.9	411	24	ABG74383	Human TNFR family
14	2163	99.7	411	20	AAW93576	Human hAP08 protei
15	2163	99.7	411	20	AAW00932	Human DR5 protein
16	2160	99.6	411	19	AAW79083	Human death domain
17	2160	99.6	411	20	AAW93608	Human killer adria
18	2160	99.6	411	21	AAE29790	Human death domain
19	2160	99.6	411	24	ABG71903	Human TRAIL recept
20	2160	99.6	411	24	ABU03488	Angiogenesis-assoc
21	2152	99.2	411	19	AAW76827	Human TR6 protein.
22	2152	99.2	411	22	AAW848348	Human tumour necro
23	2142.5	98.8	440	19	AAW79260	Tumour necrosis fa
24	2138.5	98.6	440	20	AAW05725	Tumour necrosis fa
25	2138.5	98.6	440	21	AAE01340	TNF-related apopto
26	2138.5	98.6	440	23	ABG62170	Human prostate spe
27	2135.5	98.5	440	19	AAW9284	Human TRAIL recept
28	2135.5	98.5	440	23	AAW51079	Human DR5 receptor
29	2133.5	98.4	440	24	ABG75644	Human Tango-63d pr
30	1610.5	73.6	350	20	AAW00934	Human DR5 protein
31	1597	73.6	303	19	AAW76828	Human TR6 partial
32	1597	73.6	303	22	AAW8349	Partial amino acid
33	1072	49.4	410	20	AAW93577	Human APOB protein
34	1072	49.4	468	19	AAW64483	Human DR4 protein.
35	1072	49.4	468	20	AAW31602	Human death recept
36	1072	49.4	468	20	AAW93609	Human DR4 protein.
37	1072	49.4	468	21	AAW72022	Human Death Domain
38	1072	49.4	468	21	AAH08546	Amino acid sequenc
39	1072	49.4	468	21	AAH01319	TNF-related apopto
40	1072	49.4	468	22	AAW49241	Human DR4 receptor
41	1072	49.4	468	23	AAW51078	Human TNF recepto
42	1072	49.4	468	23	AAU75063	Human TRAIL related
43	1072	49.4	468	24	ABG71901	Human TRAIL recept
44	1070	49.3	468	21	AAW72023	Human Death Domain
45	1065	49.1	418	23	ABG31491	Human Apo-2Dcr ass

ALIGNMENTS

RESULT 1	AAW79261	standard; Protein: 411 AA.
ID	AAW79261	
AC	AAW79261:	
XX		
DT	15-FEB-1999	(first entry)
XX		
DE	Tumour necrosis factor receptor related protein Tango-63e.	
XX		
KW	Tango-63e: tumour necrosis factor receptor related protein; human;	
KW	apoptosis; cancer; autoimmune disease; neurodegenerative disease.	
XX		
OS	Homo sapiens.	
XX		
PN	W09846643-A1.	
XX		
PD	22-OCT-1998.	
XX		
PF	16-APR-1998:	98MO-US07694.
XX		
PR	16-APR-1997:	97US-0843652.
XX		
PA	(MTL-) MILLENNIUM BIOTHERAPEUTICS INC.	
XX		
PI	Holzman D;	
XX		
DR	WPI: 1998-594562/50.	
XX		
PT	Isolated tumour necrosis factor related proteins - used to develop products for the diagnosis and treatment of apoptosis-related	

PT disorders, e.g. cancers, autoimmune disorders or neurodegenerative disorders

PS Claim 6; Fig 2; 88pp; English.

XX This is the amino acid sequence of Tango-63e, a new member of the human tumour necrosis factor receptor superfamily. It was deduced from a human prostate cDNA clone sequence (see AAV62673). Two different forms of Tango-63, i.e. Tango-63e and Tango-63d (see AAV79260), have been identified. These are identical with the exception of the deletion of amino acids 183-211 of Tango-63d in Tango-63e. The invention also encompasses nucleic acid molecules encoding Tango-63d and -63e, vectors containing these nucleic acid molecules, cells harboring recombinant DNA encoding Tango-63d and/or -63e, fusion proteins that include Tango-63d and/or -63e, transgenic animals that express Tango-63d and/or -63e, and recombinant knockout animals that fail to express Tango-63d and/or -63e. Methods are provided for the diagnosis and treatment of disorders associated with either an abnormally high or an abnormally low rate of apoptotic cell death. Inhibitors can be used for treating e.g. cancers, autoimmune disorders (e.g. systemic lupus erythematosus and immune-mediated glomerulonephritis), and viral infections (e.g. herpesviruses, poxviruses, and adenoviruses). Agonists can be used for treating e.g. neurodegenerative diseases, e.g. Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS), Huntington's disease, retinitis pigmentosa, spinal muscular atrophy, various forms of cerebellar degeneration, anaemia, myelodysplastic syndrome, ischemic injury, myocardial infarction, cerebral ischemia or toxin-induced injury. In addition, T cell mediated diseases, including AIDS, autoimmune diseases such as rheumatoid arthritis, and type I diabetes, septic shock, cerebral malaria, graft rejection, cytotoxicity, cachexia, and inflammation can be treated by altering the expression or activity of the polypeptides. The products can also be used for detection, diagnosis and screening assays.

CC Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 19; Length 411;

Best Local Similarity 99.8%; Pred. No. 3.3e-178; Mismatches 410; Conservative 0; Indels 1; Gaps 0;

QY 1 MEGRQNPAAASGARRHGPGRARGARGLRVKTLVLAVALVLSAESALITQDD 60
DB 1 MEGRQNPAAASGARRHGPGRARGARGLRVKTLVLAVALVLSAESALITQDD 60
QY 61 LAPQORAPQOKRSPSSGGLCPGHHISEDRDCISCKYGGDYSTHMDLFLCRLTRCD 120
DB 61 LAPQORAPQOKRSPSSGGLCPGHHISEDRDCISCKYGGDYSTHMDLFLCRLTRCD 120
QY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKRCKRTGCRGAWKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKRCKRTGCRGAWKVGDCTPMSDIECVH 180
QY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKRCKRTGCRGAWKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMKRCKRTGCRGAWKVGDCTPMSDIECVH 180
QY 181 KESGIIIGVTAAVAVLVAVFCKSLMKKVLPLYLKIGISGGGDDPERVDRSSORPGAED 240
DB 181 KESGIIIGVTAAVAVLVAVFCKSLMKKVLPLYLKIGISGGGDDPERVDRSSORPGAED 240
QY 241 NVLNEIVSILOPTQVPEQEMEVQPAEPTGVNMLSPGSEHLLPAPAEKRSQRRLLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVQPAEPTGVNMLSPGSEHLLPAPAEKRSQRRLLVPA 300
QY 301 NEGSPETLROCFDFADLVFPDSMEPLMKRLGLMDNITKAKAEAGHRTLTMTLTKW 360
DB 301 NEGSPETLROCFDFADLVFPDSMEPLMKRLGLMDNITKAKAEAGHRTLTMTLTKW 360
QY 361 VNKTRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNASAXS 411
DB 361 VNKTRDASVHTLLDALETGERLAKOKIEDHLLSSGKFMYLEGNASAXS 411

RESULT 2
AAW88410

ID AAW88410 standard; Protein: 411 AA.

AC AAW88410;

DT 26-APR-1999 (first entry)

DE Human Apo-2 ligand.

KW Apo-2 ligand; Apo-2DCR: human; tumour necrosis factor receptor; neurodegeneration; autoimmune disease; inflammation; cancer; apoptosis; therapy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Peptide 1..53

FT Protein /note= "signal peptide"

FT Domain /note= "mature protein"

FT Domain /note= "extracellular domain"

FT Domain /note= "transmembrane domain"

FT Domain /note= "intracellular domain"

FT Region /note= "cysteine-rich region"

FT Region /note= "cysteine-rich region"

FT Domain /note= "death domain"

FT Misc-difference 410

FT /label= Met, Leu

FT /note= "encoded by WTG"

XX WO9858062-A1.

XX 23-DEC-1998.

XX 12-JUN-1998; 98WO-US12456.

XX 18-JUN-1997; 97US-0878168.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;

XX Kim KO, Wood WI;

XX WPI; 1999-095340/08.

XX N-PSDB; AAW84352.

XX New Apo-2DCR polypeptide - used for modulation and diagnosis of

XX apoptosis, e.g. in neurodegeneration

XX Example 5; Page 61-62; 88pp; English.

XX This polypeptide comprises human Apo-2 ligand. The amino acid

XX sequence was deduced from a nucleotide sequence (see AAW84352)

XX produced from overlapping cDNA clones obtained from human kidney

XX and pancreatic cDNA libraries. The invention relates to Apo-2DCR

XX (see AAW8408), a novel member of the tumour necrosis factor receptor

XX family that binds to Apo-2 ligand and is involved in apoptosis.

XX Apo-2DCR polypeptides are used to modulate apoptosis of mammalian

XX cells (claimed) e.g. in the treatment of neurodegeneration,

XX autoimmune diseases and inflammation. The Apo-2DCR polypeptides

XX are optionally used in conjunction with Apo-2 ligand, the

XX bioavailability of which is increased by antibody-mediated blockade

XX of Apo-2DCR.

SO Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 20; Length 411;

Best Local Similarity 100.0%; Pred. No. 3.3e-178;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORGNAPASGARRHGGPREARGARGLRVPTLVVVAVALLVSAESALITQOD 60
DB 1 MEORGNAPASGARRHGGPREARGARGLRVPTLVVVAVALLVSAESALITQOD 60
QY 61 LAPQORAAPOQRKSSPSEGLCPGGHHISEDRDCISCKYGQDSTHWNDLFLCRLCTCD 120
DB 61 LAPQORAAPOQRKSSPSEGLCPGGHHISEDRDCISCKYGQDSTHWNDLFLCRLCTCD 120
QY 121 SGVEVLSPTCTTNTNTVQCCEEGTFREDDSPEMKRCRTGCPRMVAVGDCPTMSDIECVH 180
DB 121 SGVEVLSPTCTTNTNTVQCCEEGTFREDDSPEMKRCRTGCPRMVAVGDCPTMSDIECVH 180
QY 181 KESGIIIGTVAAVAVLVAIVAVFCKSLMKKVLPLYLGICSGGGGDDERVDRSSQRGAED 240
DB 181 KESGIIIGTVAAVAVLVAIVAVFCKSLMKKVLPLYLGICSGGGGDDERVDRSSQRGAED 240
QY 241 NVLNEIVSILQPTQVPEQEMEVQEPAPPTGVNMLSGSESHLLLEPAEAERSQRRLVPA 300
DB 241 NVLNEIVSILQPTQVPEQEMEVQEPAPPTGVNMLSGSESHLLLEPAEAERSQRRLVPA 300
QY 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKKGLMDNEIKVAKAEAGHRDTLYTMLIKW 360
DB 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKKGLMDNEIKVAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTGRDASVHTLLDLALETIGERLAKOKIEDHLLSGKFMYLEGNDSAXS 411
DB 361 VNKTGRDASVHTLLDLALETIGERLAKOKIEDHLLSGKFMYLEGNDSAXS 411

RESULT 3

AAM83321 ID AAM83321 standard; Protein; 411 AA.

XX AC AAM83321;

XX DT 16-MAR-1999 (first entry)

XX DE Human Apo-2 protein.

XX KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;

XX KM tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;

XX OS Homo sapiens.

XX FH Key location/Qualifiers

XX FT MISC-difference 410 /label= unknown

XX FT /note= "encoded by WTS"

XX XX WO9851793-A1.

XX XX 19-NOV-1998.

XX XX 14-MAY-1998; 98MO-US09704.

XX PR 09-FEB-1998; 98US-0020746.

XX PR 15-MAY-1997; 97US-0857216.

XX XX (GETH) GENENTECH INC.

XX PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KT;

XX DR WPT, 1999-045228/04.

XX DR N-PSDB; AAV72526.

XX PT Human Apo-2 polypeptide inducing apoptosis - useful to treat

XX PT conditions linked with decreased apoptosis e.g. cancer, and produce

XX PT antibodies to increase or decrease apoptosis

XX PS Claim 1; Fig 1; 134pp; English.

XX The present sequence represents human Apo-2. Apo-2 can be used
CC therapeutically to induce apoptosis in mammalian cells, and so is useful
CC to treat conditions associated with decreased apoptosis e.g. cancer.
CC Apo-2 is believed to be a tumour necrosis factor (TNF) receptor
CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It
CC can be used to identify agents activating Apo-2, useful to treat
CC mammalian cancer cells, and to produce Apo-2 chimeras useful
CC therapeutically (e.g. those containing immunoglobulin sequences can be
CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope
CC tag polypeptide allow Apo-2 detection and purification using anti-tag
CC antibodies). It can be used to produce antibodies which can be combined
CC with a (particularly pharmaceutically acceptable) carrier in compositions
CC or used to produce dimeric molecules (especially homodimeric molecules
CC comprising first and second Apo-2 antibodies). Agonistic (especially
CC single-chain) antibodies can be administered to induce apoptosis in
CC mammalian cancer cells, and antagonistic antibodies used to block
CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2
CC antibodies may also be used diagnostically e.g. to detect Apo-2
CC expression in cells/tissues and in Apo-2 purification.

XX SQ Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 20; Length 411;

Best Local Similarity 100.0%; Pred. No. 3.3e-178;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORGNAPASGARRHGGPREARGARGLRVPTLVVVAVALLVSAESALITQOD 60

DB 1 MEORGNAPASGARRHGGPREARGARGLRVPTLVVVAVALLVSAESALITQOD 60

QY 61 LAPQORAAPOQRKSSPSEGLCPGGHHISEDRDCISCKYGQDSTHWNDLFLCRLCTCD 120

DB 61 LAPQORAAPOQRKSSPSEGLCPGGHHISEDRDCISCKYGQDSTHWNDLFLCRLCTCD 120

QY 121 SGVEVLSPTCTTNTNTVQCCEEGTFREDDSPEMKRCRTGCPRMVAVGDCPTMSDIECVH 180

DB 121 SGVEVLSPTCTTNTNTVQCCEEGTFREDDSPEMKRCRTGCPRMVAVGDCPTMSDIECVH 180

QY 181 KESGIIIGTVAAVAVLVAIVAVFCKSLMKKVLPLYLGICSGGGGDDERVDRSSQRGAED 240

DB 181 KESGIIIGTVAAVAVLVAIVAVFCKSLMKKVLPLYLGICSGGGGDDERVDRSSQRGAED 240

QY 241 NVLNEIVSILQPTQVPEQEMEVQEPAPPTGVNMLSGSESHLLLEPAEAERSQRRLVPA 300

DB 241 NVLNEIVSILQPTQVPEQEMEVQEPAPPTGVNMLSGSESHLLLEPAEAERSQRRLVPA 300

QY 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKKGLMDNEIKVAKAEAGHRDTLYTMLIKW 360

DB 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKKGLMDNEIKVAKAEAGHRDTLYTMLIKW 360

QY 361 VNKTGRDASVHTLLDLALETIGERLAKOKIEDHLLSGKFMYLEGNDSAXS 411

DB 361 VNKTGRDASVHTLLDLALETIGERLAKOKIEDHLLSGKFMYLEGNDSAXS 411

RESULT 4 AAY55805 ID AAY55805 standard; Protein; 411 AA.

XX AC AAY55805;

XX DT 29-FEB-2000 (first entry)

XX DE Human Apo-2 polypeptide.

XX KW Apo-2 polypeptide; immunization; antigen; polyclonal antibody; cancer;

XX KM monoclonal antibody; Apo-2L receptor; therapy; apoptosis; autoimmune;

XX KM immune-mediated cell death; neurodegenerative; inflammatory.

XX OS Homo sapiens.

Key Location/Qualifiers
FT Misc-difference 410 /label= unknown
FT /note= "encoded by WTG"
XX W09964461.A2.
XX 16-DEC-1999.
XX 10-JUN-1999; 99W0-US13197.
XX 12-JUN-1998; 98US-0096637.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI: 2000-097520/08.
XX N-PSDB; AA239630.
XX Preparation of antibodies using 2 or more different antigens, used for
PT producing antibodies against Apo-2 ligand receptors useful for inducing
PT apoptosis, particularly in cancer cells
XX Disclosure; Fig 5; 57pp; English.
XX The invention provides a method for producing antibodies (Abs) by
CC immunizing an animal with at least two different antigens. The method
CC comprises: (a) immunizing an animal with at least two different antigens,
CC to generate polyclonal Abs against each antigen in the animal; (b)
CC preparing monoclonal Abs (MAbs) using immune cells of the above animal;
CC and(c) screening the MAbs to identify one or more MAbs which bind to each
CC antigen. The Abs obtained are Apo-2L receptor (ant)agonists and can be
CC used for therapy. The Apo-2L receptor Abs can be used for enhancing
CC immune-mediated cell death in cells expressing Apo-2L receptors.
CC Agonistic Abs which specifically cross-react with 2 or more different
CC Apo-2L receptors can be used for inducing apoptosis in mammalian cancer
CC cells. Antagonistic Abs can be used for blocking apoptosis, e.g. in
CC neurodegenerative disease, or to block potential autoimmune/inflammatory
CC effects of Apo-2 resulting from NF-approx KB activation. The Abs can also
CC be used for detection, diagnosis and affinity purification. The method
CC can reduce the number of animals that need to be immunized and sacrificed
CC in order to make 2 or more MAbs with differing antigen-binding
CC specificities. The present sequence represents a human Apo-2 polypeptide.
XX
XX Sequence 411 AA;
SO
Query Match 99.9%; Score 2167; DB 21; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORGONAPASAGRRKRRGPPRRARGARGLRVPKTLVVAAYLLVLSAESLITQOD 60
DB 1 MEORGONAPASAGRRKRRGPPRRARGARGLRVPKTLVVAAYLLVLSAESLITQOD 60
QY 61 LAPQARAPOOKRSSPSEGLCPGCHHTSEDRDCISCKYQADYSTHNDLFLCJRCTCD 120
DB 61 LAPQARAPOOKRSSPSEGLCPGCHHTSEDRDCISCKYQADYSTHNDLFLCJRCTCD 120
QY 121 SGEVELSPCTTTRNTVOCCEGTFREDDSPBCKKCTGCGRCGNKAVGDCPTMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVOCCEGTFREDDSPBCKKCTGCGRCGNKAVGDCPTMSDIECVH 180
QY 181 KESGIIIGVVAAYVVLVAAYVCKSLMKVLPYLKICSGGGDPRVRSSQRPAAED 240
DB 181 KESGIIIGVVAAYVVLVAAYVCKSLMKVLPYLKICSGGGDPRVRSSQRPAAED 240
QY 241 NVLINEIYSILOPTQVPEQEMEVOPAPPTGNNMLSPESSEHLEPAEASQRRLLVPA 300
DB 241 NVLINEIYSILOPTQVPEQEMEVOPAPPTGNNMLSPESSEHLEPAEASQRRLLVPA 300
QY 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKRLGLMONEIVAKAEAGHDTLYTMLIKW 360
DB 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKRLGLMONEIVAKAEAGHDTLYTMLIKW 360

DB 301 NEGDPTETLRQCFDDFADLVFPDSWEPMLMKRLGLMONEIVAKAEAGHDTLYTMLIKW 360
QY 361 VNKGRASVHTLLDALETGERLAKOKIEDHLLSSGKPMYLEENADSAXS 411
DB 361 VNKGRASVHTLLDALETGERLAKOKIEDHLLSSGKPMYLEENADSAXS 411
RESULT 5
AAU04038
ID AAU04038 standard; Protein: 411 AA.
AC AAU04038;
XX 23-OCT-2001 (first entry)
DT Human apoptotic protein, Apo-2.
DE Human; Apo-2; Apo-2L receptor; immunogen; monoclonal antibody;
XX cancer; tumour; apoptosis; lymphoma; blastoma; sarcoma; leukaemia;
KW 3H3.14.5.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 410 /label= OTHER
FT /note= "Other= Leu Or Met"
XX US6252050-B1.
XX 26-JUN-2001.
XX 10-JUN-1999; 99US-0329633.
XX 12-JUN-1998; 98US-0089253.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI: 2001-424490/45.
XX N-PSDB; AAS07626.
XX Novel human monoclonal antibody for inducing apoptosis in mammalian
PT cancer cells, specifically cross-reacts with two or more different
PT Apo-2 ligand receptors
XX
XX Example 1; Fig 5; 29pp; English.
PS The sequence represents human Apo-2, an apoptotic protein used as an
XX immunogen to make the monoclonal antibodies of the invention. The
XX invention relates to an isolated antibody which specifically cross-reacts
XX with two or more different Apo-2 ligand (Apo-2L) receptors. Apoptosis by
XX monoclonal antibody 3H3.14.5 after crosslinking with anti-mouse Ig was
XX tested. Human 9D cells in complete RPMI medium were added. Cells were
XX incubated with the monoclonal antibody in 100 micro on ice for 15
XX minutes. Cells were then incubated with goat anti-mouse IgG FC complete
XX RPMI medium overnight at 37 degrees C. After washing once with PBS, cells
XX were resuspended in PBS containing 0.5% BSA and incubated with FITC-
XX Annexin and propidium iodide for 15 minutes in the dark. Dead cells were
XX detected by FACScan. The 3H3.14.5 antibody was able to inhibit apoptosis
XX induced by interaction between Apo-2L and Apo-2. This antibody was
XX further capable of inducing apoptosis of 9D cells in the presence of an
XX anti-Fc antibody to cross-link antibodies. The antibodies are useful for
XX inducing apoptosis in mammalian cancer cells for treating cancer
XX including carcinoma, lymphoma, blastoma, sarcoma and leukaemia, and are
XX useful in diagnostic assays for their antigen, e.g. detecting its
XX expression in specific cells, tissues or serum and for affinity
XX purification of antigen from recombinant cell culture or natural sources.
XX
XX Sequence 411 AA;
SO
Query Match 99.9%; Score 2167; DB 22; Length 411;

Best Local Similarity 100.0%; Pred. No. 3.3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEQRGONAPASGARRKRGPGPREARARGLRPKTLVVAVALLVSAESALITQOD 60
DB 1 MEQRGONAPASGARRKRGPGPREARARGLRPKTLVVAVALLVSAESALITQOD 60
OY 61 LAPQORAAPOOKRSSPSEGLCPRGHNSIEGRDICSKYQDSTHNNDLFLCRLTRCD 120
DB 61 LAPQORAAPOOKRSSPSEGLCPRGHNSIEGRDICSKYQDSTHNNDLFLCRLTRCD 120
OY 121 SGEVELSPCTTTRNTVCQCEGTFREEDSPDMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCQCEGTFREEDSPDMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
OY 181 KESGIITGVVAANVLVAFAVCKSLMKVLPYLKICSGGGDPRVRRSSORPAED 240
DB 181 KESGIITGVVAANVLVAFAVCKSLMKVLPYLKICSGGGDPRVRRSSORPAED 240
OY 241 NVLNEIVSIQPTQVPEQEMEOEPAPETGVNMLSPSEHLLPEPAERSQRRRLVPA 300
DB 241 NVLNEIVSIQPTQVPEQEMEOEPAPETGVNMLSPSEHLLPEPAERSQRRRLVPA 300
OY 301 NEGDPTETLRQCFDDEADLVPPDSWEPMLMKLGIMDNEIKVAKAEAGHSDTLVTMLIKW 360
DB 301 NEGDPTETLRQCFDDEADLVPPDSWEPMLMKLGIMDNEIKVAKAEAGHSDTLVTMLIKW 360
OY 361 VNTGRASVHTLLDALETGERLAKOKIEDHLLSSKRFMYLEGNADSAXS 411
DB 361 VNTGRASVHTLLDALETGERLAKOKIEDHLLSSKRFMYLEGNADSAXS 411

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RESULT 6
AAB73442
ID AAB73442 standard; Protein: 411 AA.
XX
AC AAB73442:
XX
DT 25-JUN-2001 (first entry)
XX
DE Human Apo-2 receptor precursor, SEQ ID NO:2.
XX
KW Human Apo-2 receptor; caspase-dependent apoptosis induction;
KW programmed cell death; pro-apoptotic; death domain;
KW agonistic antibody; nuclear factor kappa B;
KW NF-kappa-B activation; cancer; tumour; lung cancer;
KW colon cancer; glioma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..53
FT Protein /note- "Signal peptide"
FT /note- "Mature human Apo-2 receptor"
FT Domain 54..182
FT /note- "Extracellular domain. This domain is
FT alternatively residues 1-182, or residues 1-130"
FT Disulfide-bond 81..94
FT Domain 96..137
FT /note- "Cysteine-rich pseudorepeat domain #1"
FT Disulfide-bond 97..113
FT Binding-site 106
FT /note- "Binds Apo-2L"
FT Binding-site 112
FT /note- "Binds Apo-2L"
FT Disulfide-bond 116..129
FT Disulfide-bond 119..137
FT Domain 138..183
FT /note- "Cysteine-rich pseudorepeat domain #2"
FT Disulfide-bond 139..153
FT Disulfide-bond 156..170
FT Disulfide-bond 160..178

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FT Domain 183..208
FT /note- "Transmembrane domain"
FT Domain 209..411
FT /note- "Intracellular domain"
FT Domain 324..391
FT /note- "Death domain"
FT Misc-difference 410
FT /label= Met, Leu
FT /note- "Encoded by WTG. This residue is Met in kidney
FT Apo-2, and is Leu in pancreatic Apo-2."
XX
XX WO200119861-A2.
XX
XX 22-MAR-2001.
XX
XX 14-SEP-2000; 2000WO-US25436.
XX
XX 15-SEP-1999; 99US-0396710.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Chuntherapai A, Kim KJ;
XX
XX WPI: 2001-266005/27.
XX
XX N-PSDB: AAF84481.
XX
XX
XX Inducing apoptosis in mammalian cells for treating cancer, comprises
XX exposing mammalian cells or cancer cells expressing Apo-2 receptor, to
XX Apo-2 agonist antibody.
XX
XX Example 1; Fig 1; 90pp; English.
XX
XX
XX The invention relates to a method for inducing apoptosis in mammalian
XX cells which express the Apo-2 receptor protein (AAB73442, AAB73443).
XX The method involves exposing the cells to an Apo-2 agonistic antibody,
XX which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor
XX (also referred to simply as Apo-2) is a member of the tumour
XX necrosis factor receptor (TNFR) family, and its natural ligand is the
XX Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able
XX to trigger caspase-dependent apoptosis, and is also able to activate
XX NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an
XX approximately 45 kD type I transmembrane protein, and contains a death
XX domain in the cytoplasmic region (residues 324-392). It exhibits
XX significantly more sequence identity to the apoptosis-linked receptor
XX DR4, which also binds Apo-2L, than other apoptosis-associated proteins.
XX The Apo-2 receptor agonist monoclonal antibodies used in the method of
XX the invention are 3F11.39.7, 3H3.14, 5, 305.1.10 and 3H1.18.10. The
XX method of the invention is used to induce apoptosis in Apo-2-expressing
XX cells, particularly cancer cells. It may therefore be used for treating
XX mammalian cancers, especially lung cancer, colon cancer and glioma.
XX The present sequence represents human Apo-2 as encoded by cDNA isolated
XX in an exemplification of the invention.
XX Note: The present sequence differs from the human Apo-2 receptor
XX precursor given in AAB73443 in that residue 410 of this sequence can be
XX Met or Leu, rather than Leu.
XX
XX
XX Sequence 411 AA:

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Query Match 99.9%; Score 2167; DB 22; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEQRGONAPASGARRKRGPGPREARARGLRPKTLVVAVALLVSAESALITQOD 60
DB 1 MEQRGONAPASGARRKRGPGPREARARGLRPKTLVVAVALLVSAESALITQOD 60
OY 61 LAPQORAAPOOKRSSPSEGLCPRGHNSIEGRDICSKYQDSTHNNDLFLCRLTRCD 120
DB 61 LAPQORAAPOOKRSSPSEGLCPRGHNSIEGRDICSKYQDSTHNNDLFLCRLTRCD 120
OY 121 SGEVELSPCTTTRNTVCQCEGTFREEDSPDMCRKCTGCPRGWVKVGDCTPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCQCEGTFREEDSPDMCRKCTGCPRGWVKVGDCTPMSDIECVH 180

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RESULT 8
ABG31490
ID ABG31490 standard; Protein: 411 AA.
XX
AC ABG31490;
XX
DT 21-NOV-2002 (first entry)
XX
DE Amino acid sequence for human Apo-2.
XX
KW Human; Apo-2Dcr; Apo-2 ligand; programmed cell death; apoptosis;
neurodegenerative disease; autoimmune; inflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 410
FT /label= "Leu, Met
FT /note= "Encoded by WTG"
XX
PN US2002102706-A1.
XX
PD 01-AUG-2002.
XX
PF 21-JUN-2001; 2001US-0887879.
XX
PR 18-JUN-1997; 97US-049911P.
PR 12-JUN-1998; 98US-0096500.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Chantharapai A, Gurney A, Kim KJ, Wood WI;
DR WPI; 2002-697823/75.
DR N-PSDB; ABS53575.
XX
PT Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in
mammalian cells -
XX
PS Example 5; Fig 8; 58pp; English.
XX
CC The present invention relates to the isolation of novel human
polypeptides, designated Apo-2Dcr, and the polynucleotide sequences
encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is
useful for modulating programmed cell death or apoptosis in
mammalian cells. Apo-2Dcr can be used to produce apo-2Dcr antibodies
which are useful therapeutically, and can cross-react with other
receptors for Apo-2 ligand to block excessive apoptosis in
neurodegenerative diseases, or to block potentially autoimmune
or inflammatory effects. Apo-2Dcr antibodies are also useful in
immunohistochemistry staining assays or diagnostic assays for
Apo-2Dcr, e.g. detecting it's expression in specific cells, tissues
or serum, and for the affinity purification of Apo-2Dcr from
recombinant cell culture or natural sources. The present sequence
represents human Apo-2.
XX
SQ Sequence 411 AA;
Query Match 99.9%; Score 2167; DB 23; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MEORGNAAPASGARRKHGEPREARCARGLRVPKTLVVAVALLVSAESALITQOD 60
DB 1 MEORGNAAPASGARRKHGEPREARCARGLRVPKTLVVAVALLVSAESALITQOD 60
OY 61 LAPQRAAPQOKSSPEGLCPPEGHHSDEGRDICKYQODSTHNDLLFCRCRCD 120
DB 61 LAPQRAAPQOKSSPEGLCPPEGHHSDEGRDICKYQODSTHNDLLFCRCRCD 120
OY 121 SGEVLSPTCTTTRNTVQCCEGTFRFEDSDPMCKRCKTCGPRGNVKGDCPTWSDIECVH 180
DB 121 SGEVLSPTCTTTRNTVQCCEGTFRFEDSDPMCKRCKTCGPRGNVKGDCPTWSDIECVH 180
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DB 121 SGEVLSPTCTTTRNTVQCCEGTFRFEDSDPMCKRCKTCGPRGNVKGDCPTWSDIECVH 180
OY 181 KESGIITGVAAVAVLVIAVFCVCKSLMKRVLPYKICGGGGDPERRVSSQRPQAE 240
DB 181 KESGIITGVAAVAVLVIAVFCVCKSLMKRVLPYKICGGGGDPERRVSSQRPQAE 240
OY 241 NVLNEIVSILOPTQVPEOMEVQEPAPPTGVNMLSPGSEHLLLEPAEERSQRRLLVPA 300
DB 241 NVLNEIVSILOPTQVPEOMEVQEPAPPTGVNMLSPGSEHLLLEPAEERSQRRLLVPA 300
OY 301 NEGDPTETLRQCEDEADLVPPDSWEPLMKRLGIMDNEIVAKAAAGHRDLYTMLIKW 360
DB 301 NEGDPTETLRQCEDEADLVPPDSWEPLMKRLGIMDNEIVAKAAAGHRDLYTMLIKW 360
OY 361 VNKTGRASVHTLLDALETGERLAKKIDHLLSSKRYVLDGNADSAXS 411
DB 361 VNKTGRASVHTLLDALETGERLAKKIDHLLSSKRYVLDGNADSAXS 411
RESULT 9
AAM51080
ID AAM51080 standard; Protein: 411 AA.
XX
AC AAM51080;
XX
DT 30-MAY-2002 (first entry)
XX
DE Human DR5 receptor.
XX
KW DR5 receptor; receptor; Apo-2 ligand; Apo-2L; agonist; human;
apoptosis; colorectal cancer; tumour; antitumour; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 410
FT /note= "unidentified amino acid residue"
XX
PN W020020975-A2.
XX
PD 07-FEB-2002.
XX
PF 27-JUL-2001; 2001WO-US23691.
XX
PR 27-JUL-2000; 2000US-221256P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Escandon E, Fox JA, Kelley SK, Xiang H;
DR WPI; 2002-268997/31.
XX
XX
PT Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
inhibitor class, and Apo-2 ligand receptor agonist for enhancing
apoptosis in mammalian cells, or for treating cancer in a mammal
XX
PS Disclosure; Page 83-84; 84pp; English.
XX
CC The present sequence is that of human DR5 receptor, a receptor for
Apo-2 ligand (Apo-2L). An alternative sequence for the D5 receptor
is given in AAM51079. The invention relates to methods of inducing
apoptosis in mammalian cells, and especially to the use of Apo-2L
receptor agonists and CPT-11 (a chemotherapeutic agent of the
topoisomerase I inhibitor class) to synergistically induce apoptosis
in mammalian cells, in particular mammalian cancer cells, and
especially colorectal cancer cells (claimed). The cells may be in
cell culture or in a mammal, e.g. a mammal suffering from cancer or
a condition in which induction of apoptosis in the cells is
desirable. A claimed method of treating cancer in a mammal
comprises administering CPT-11 and Apo-2L receptor agonist, where
the CPT-11 is administered about 6-72 hours prior to administration
of the Apo-2L receptor agonist. Preferred Apo-2L receptor agonists
include Apo-2L and anti-DR4 or anti-DR5 receptor antibodies.
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CC especially chimeric, humanised or human antibodies. Exposure of
CC the cancer cells to CPT-11 and Apo-2L receptor agonist leads to
CC upregulation of DR4 and DR5 receptors, directing the cells towards
CC an apoptotic pathway rather than cell cycle arrest and possible DNA
CC repair, thus providing enhanced antitumour activity.

XX Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 23; Length 411;
Best Local Similarity 100.0%; Pred. No. 3,3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORQONAPASGARRHGPGRARARGLRVKTLVVAALLVSAESALITQOD 60
DB 1 MEORQONAPASGARRHGPGRARARGLRVKTLVVAALLVSAESALITQOD 60
QY 61 LAPQORAPQOKRSSPSGICPPGHHSIEDGRDCISCKYGGDYSTHNDLFLCRLCTCD 120
DB 61 LAPQORAPQOKRSSPSGICPPGHHSIEDGRDCISCKYGGDYSTHNDLFLCRLCTCD 120
QY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMCKRCRTGCPRGWYKVGDCIPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMCKRCRTGCPRGWYKVGDCIPMSDIECVH 180
QY 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSQRPAGD 240
DB 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSQRPAGD 240
QY 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300
QY 301 NEGDPTETLRQCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360
DB 301 NEGDPTETLRQCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 10

AAU76947 standard; Protein: 411 AA.

AAU76947;

05-JUN-2002 (first entry)

Human Apo2 protein.

DE Human Apo2 protein.
XX Apo-2; human; antibody; Apo-2L; cytostatic; neuroprotective;
KW antiinflammatory; immunosuppressive; apoptosis; cancer;
KW neurodegenerative disease; autoimmune disease; inflammatory disease.
XX Homo sapiens.

OS Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 410
FT /label- Ieu, Met
FT /note- "This represents a naturally occurring
FT variant of the apo-2 protein"
XX US2002004227-A1.

10-JAN-2002.

09-APR-2001; 2001US-0828739.

12-JUN-1998; 98US-089253P.
PR 10-JUN-1999; 99US-0329633.

XX (GETH) GENE TECH INC.

XX Ashtkenazi AJ, Chuntharapat A, Kim KJ;
PI WPI: 2002-239130/29.
XX N-PSDB; ABR10298.
DR

PT Novel nucleic acid encoding antibody that specifically cross-reacts
PT with two or more different Apo-2 ligand receptors, useful for preparing
PT the antibody by recombinant techniques
PS Disclosure: Fig 5; 30pp: English.

XX This invention relates to an isolated nucleic acid comprising DNA
CC encoding an antibody which specifically cross-reacts with two or more
CC different Apo-2 and Apo-2L ligand (Apo-2L) receptors. The nucleotide
CC sequences of the invention are useful for preparing anti-Apo2 antibodies
CC by recombinant techniques, these antibodies may be employed to activate
CC or stimulate apoptosis in cancer cells. The Apo-2L receptor antibodies
CC are useful for enhancing immune-mediated cell death in cells expressing
CC Apo-2L receptors. The antagonistic Apo-2L receptor antibodies may be
CC used to block excessive apoptosis (neurodegenerative disease) or to
CC block autoimmune/inflammatory effects of Apo-2 resulting from NFkBpAB
CC activation. The antibodies encoded by the nucleotide sequences of the
CC invention can also be used in diagnostic assays for their antigen e.g.,
CC detecting its expression in specific cells, tissues or serum. The
CC present sequence represents the human Apo-2 protein sequence used to
CC generate anti-Apo-2 antibodies using the method of the invention. This
CC sequence represents both naturally occurring natural variants of this
CC cDNA (Leucine or methionine at residue 410).

XX Sequence 411 AA:

Query Match 99.9%; Score 2167; DB 23; Length 411;
Best Local Similarity 100.0%; Pred. No. 3,3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORQONAPASGARRHGPGRARARGLRVKTLVVAALLVSAESALITQOD 60
DB 1 MEORQONAPASGARRHGPGRARARGLRVKTLVVAALLVSAESALITQOD 60
QY 61 LAPQORAPQOKRSSPSGICPPGHHSIEDGRDCISCKYGGDYSTHNDLFLCRLCTCD 120
DB 61 LAPQORAPQOKRSSPSGICPPGHHSIEDGRDCISCKYGGDYSTHNDLFLCRLCTCD 120
QY 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMCKRCRTGCPRGWYKVGDCIPMSDIECVH 180
DB 121 SGEVELSPCTTTRNTVCCCEGTFRREDSPEMCKRCRTGCPRGWYKVGDCIPMSDIECVH 180
QY 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSQRPAGD 240
DB 181 KESGIIIGVTAAVAVLVAVFVCKSLMKKVLPLYLKGICSGGGGDPERVDSSQRPAGD 240
QY 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300
DB 241 NVLNEIVSILOPTQVPEQEMEVQEPAPETGVNMLSPGSEHLLPEPAERQORRLVPA 300
QY 301 NEGDPTETLRQCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360
DB 301 NEGDPTETLRQCFDFADLVFPDSMEPLMRKLGIMDNEIKAKAEAGHRDTLYTMLIKW 360
QY 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
DB 361 VNKTRGRDASVHTLLDALETIGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 11

ABB09602 standard; Protein: 411 AA.

ABB09602;

29-MAY-2002 (first entry)

DE	Amino acid sequence of human Apo-2 polypeptide.
XX	
KW	Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
KM	caspase; apoptosis; cancer.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..53
FT	/note= "signal peptide"
FT	Protein 54..411
FT	/note= "mature protein"
FT	Domain 183..208
FT	/note= "putative transmembrane domain"
FT	Domain 324..391
FT	/note= "death domain"
FT	Misc-difference 410
FT	/note= "unspecified amino acid encoded by WNG"
XX	
PN	US6342369-B1.
PD	
PD	29-JAN-2002.
XX	
PE	14-MAY-1998; 98US-0079029.
XX	
PR	15-MAY-1997; 97US-046615P.
PR	09-FEB-1998; 98US-074119P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Ashkenazi AJ;
XX	
DR	WPI: 2002-224941/28.
DR	N-PSDB: ABL41729.
XX	
PT	New nucleic acids encoding an Apo-2 ligand, useful for activating or stimulating apoptosis in cancer cells, thus especially useful in the treatment of cancer, or in enhancing immune-mediated cell death .
XX	
PS	Example 1; Fig 2A; 68pp; English.
XX	
CC	The present sequence represents human Apo-2 polypeptide. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural sources.
CC	
CC	
CC	
CC	
CC	
CC	
XX	
SO	Sequence 411 AA:
QY	Query Match 99.9%; Score 2167; DB 23; Length 411;
Db	Best Local Similarity 100.0%; Pred. No. 3.3e-178;
Matches	411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MEQGQNAPASGARRKRGPEPRARCARPELRVPKTIVLVAAVLVSASALITQD 60
Db	1 MEQGQNAPASGARRKRGPEPRARCARPELRVPKTIVLVAAVLVSASALITQD 60
QY	LAPORRAPOOKRASPSSEGLCPPEGHHSSEDRDCISCKYGGDYSTHMNDLFCRCRTPCD 120
Db	61 LAPORRAPOOKRASPSSEGLCPPEGHHSSEDRDCISCKYGGDYSTHMNDLFCRCRTPCD 120
QY	121 SGEVELSPCTTRNTATVCCEEGTFREEDSPEMCRKCRRTGCRGMVKYGDTWPMSDIECVH 180
Db	121 SGEVELSPCTTRNTATVCCEEGTFREEDSPEMCRKCRRTGCRGMVKYGDTWPMSDIECVH 180
QY	181 KESGIIGTVAAVLYAVFVCSLSLMKKVLPFLKGICSGGGGDPEVYRSSQRGAED 240
Db	181 KESGIIGTVAAVLYAVFVCSLSLMKKVLPFLKGICSGGGGDPEVYRSSQRGAED 240

Db	181	KESGIITGVYAAAVLVIAVFCVSLMKKVLPLTKIGICSGGGDPEVDRSSQRPAED	240
Oy	241	NVLNEIVSILOPTGVPEQGEVQEPAPETGVNMLSPGSEHLLPAPAEERSQRRLLVPA	300
Db	241	NVLNEIVSILOPTGVPEQGEVQEPAPETGVNMLSPGSEHLLPAPAEERSQRRLLVPA	300
Oy	301	NEGPPTETLRCCFEDFDVLPFDSDWEPMLMKRLGLMDNEIKAKAEAGHRPTLTMTLKW	360
Db	301	NEGPPTETLRCCFEDFDVLPFDSDWEPMLMKRLGLMDNEIKAKAEAGHRPTLTMTLKW	360
Oy	361	VNKGGRDASVHTLLDALETLEGRILAKOKIEDHLLSSGKFWYLEGNADSAXS	411
Db	361	VNKGGRDASVHTLLDALETLEGRILAKOKIEDHLLSSGKFWYLEGNADSAXS	411
RESULT 12			
AC	ABG75645	ABG75645 standard; Protein: 411 AA.	
XX	ABG75645;		
XX	29-APR-2003 (first entry)		
DE	Human Tango-63e protein.		
XX	Human; inflammation; viral encephalitis; meningitis;		
KW	multiple sclerosis; stroke; Alzheimer's disease; polycythaemia vera;		
KW	hyperproliferative myeloid disease; chronic myelogenous leukaemia;		
KW	HIV infection; autoimmune disease; systemic lupus erythematosus;		
KW	rheumatoid arthritis; type I diabetes; septic shock; graft rejection;		
KW	cerebral malaria; cachexia; cardiovascular disorder; angina pectoris;		
KW	myocardial infarction; hypertension; atherosclerosis;		
KW	haematologic disease; aplastic anaemia; chronic neutropenia;		
XX	myelodysplastic syndrome; Tango-63e; chromosome 8.		
OS	Homo sapiens.		
XX	US2002160446-A1.		
PN	31-OCT-2002.		
XX	16-MAR-2001; 2001US-0811088.		
PF	14-NOV-2000; 2000US-0712726.		
XX	(HOLT/) HOLTZMAN D A.		
XX	(GEAR/) GEARING D P.		
PA	(PANY/) PAN Y.		
XX	Holtzman DA, Gearing DP, Pan Y;		
PI	WPI: 2003-265759/26.		
XX	N-PSDB: ABX11269.		
DR	New isolated nucleic acid molecule encoding thymotaxin (Tango-45),		
PT	Tango-63d, Tango-67e, Tango-67, or huchordrin polypeptide, useful for		
PT	diagnosing and treating disorders, e.g. cancer, inflammation, stroke or		
PT	diabetes		
XX	Claim 9; Fig 4; 79pp: English.		
PS	The invention relates to an isolated nucleic acid molecule encoding		
XX	thymotaxin (also known as Tango-45), Tango-63d, Tango-637e, Tango-67,		
CC	or huchordrin polypeptide, including sequences 90% identical to them,		
CC	fragments of at least 15 nucleotides and allelic variants. Also		
CC	included are a host cell or a non-mammalian host cell containing the		
CC	novel nucleic acid, the encoded polypeptides (or allelic variants,		
CC	sequences 90% identical or fragments), an antibody or antibody		
CC	substance that selectively binds with one of the proteins, and		
CC	identifying a compound that binds with the proteins and/or modulates		
CC	the proteins' activity. Thymotaxin is a member of the C-C family of		
CC	chemokines, Tango-63e and -d are members of the tumour necrosis		
CC	factor superfamily, Tango-67 is a growth factor family member. The		

Thymotaxin gene is located on human chromosome 16 and Tango-63 on chromosome 8. The nucleic acid molecules and polypeptides are useful for diagnosing and treating disorders associated with aberrant expression or activity of the nucleic acid or polypeptide, such as inflammation (e.g. viral encephalitis, viral or bacterial meningitis, multiple sclerosis, stroke or Alzheimer's disease), hyperproliferative myeloid disease (e.g. chronic myelogenous leukemia or polycythemia vera), HIV infection, autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, type I diabetes, septic shock, graft rejection, cerebral malaria or cachexia), cardiovascular disorders (e.g. angina pectoris, myocardial infarction, hypertension or atherosclerosis), or hematologic diseases (e.g. aplastic anaemia, chronic neutropenia or myelodysplastic syndromes). The polypeptides are useful for generating antibodies, which are therapeutically useful. The nucleic acid molecules are useful as primers or probes to detect mutations or polymorphisms in the gene. The methods are useful for identifying compounds that modulate the expression or activity of the polypeptide. The present sequence represents Tango-63e.

Sequence 411 AA:

Query Match 99.9%: Score 2167; DB 24; Length 411;
Best Local Similarity: 99.8%; Pred. No. 3.3e-178;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MEORGNAPASGARRHGPGRARGARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
    |||||||
DB 1 MEORGNAPASGARRHGPGRARGARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
OY 61 LAPQORAPQOKRSSPSEGLCPGHHISEDRDICSCKYGDYSTHWNDDLLFCLRCTCD 120
    |||||||
DB 61 LAPQORAPQOKRSSPSEGLCPGHHISEDRDICSCKYGDYSTHWNDDLLFCLRCTCD 120
OY 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCPGKRGWKVGDCTPWSIDICVH 180
    |||||||
DB 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCPGKRGWKVGDCTPWSIDICVH 180
OY 181 KESGIIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDDPERVDRSSORPGAED 240
    |||||||
DB 181 KESGIIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDDPERVDRSSORPGAED 240
OY 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSORRLVPA 300
    |||||||
DB 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSORRLVPA 300
OY 301 NEGPTEFLRCCFDPAFLVPDSEWPELMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
    |||||||
DB 301 NEGPTEFLRCCFDPAFLVPDSEWPELMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
OY 361 VNKTRGRASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411
    |||||||
DB 361 VNKTRGRASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSAMS 411

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RESULT 13

ABG74383 ID ABG74383 standard; Protein: 411 AA.

XX ABG74383;

XX 11-APR-2003 (first entry)

DE Human TNFR family related protein Apo-2.

KW Human: apo-2; tumour necrosis factor family; TNFR; gene therapy;

KM apoptosis; tissue-specific typing; affinity purification;

XX Competitive-type receptor binding assay.

OS Homo sapiens.

XX Key

FT Domain

Location/Qualifiers
1..182

FT Domain /label= Extracellular_domain_1
FT 54..182
FT /label= Extracellular_domain_2
FT Domain 324..391
FT /label= Isolated_death_domain
FT Misc-difference 410
FT /note= "Encoded by WNG"

US2002150985-A1.
17-OCT-2002.

02-NOV-2001; 2001US-0052798.

15-MAY-1997; 97US-046615P.
PR 09-FEB-1998; 98US-074119P.
PR 14-MAY-1998; 98US-0079029.

(GERTH) GENENTECH INC.

Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;

WPL; 2003-198287/19.

N-PSDB; ABX16403.

New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, or in generating antibodies against Apo-2.

Claim 4; Fig 1A-C; 64pp; English.

The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays when labeled with, for instance, radiolodine, enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a diagnostic for tissue-specific typing. This is the amino acid sequence of the novel Apo-2 protein of the invention, thought to be a member of the tumour necrosis factor receptor (TNFR) family.

Sequence 411 AA:

Query Match 99.9%: Score 2167; DB 24; Length 411;
Best Local Similarity: 100.0%; Pred. No. 3.3e-178;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEORGNAPASGARRHGPGRARGARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
    |||||||
DB 1 MEORGNAPASGARRHGPGRARGARPGRLRPVKTLYLVAAVLLVSAESALITQOD 60
OY 61 LAPQORAPQOKRSSPSEGLCPGHHISEDRDICSCKYGDYSTHWNDDLLFCLRCTCD 120
    |||||||
DB 61 LAPQORAPQOKRSSPSEGLCPGHHISEDRDICSCKYGDYSTHWNDDLLFCLRCTCD 120
OY 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCPGKRGWKVGDCTPWSIDICVH 180
    |||||||
DB 121 SGEVELSCTTTRNTVCCCEGTREEDSPMCRCRCRCPGKRGWKVGDCTPWSIDICVH 180
OY 181 KESGIIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDDPERVDRSSORPGAED 240
    |||||||
DB 181 KESGIIIGVTVAAVLLVAVFCKSLMKKVLPLYLKGISGGGDDPERVDRSSORPGAED 240
OY 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSORRLVPA 300
    |||||||
DB 241 NVLNEIYSIILOPTQVPEQEMEVOEPAEPTGVNMLSPGSEHLLPEPAERSORRLVPA 300
OY 301 NEGPTEFLRCCFDPAFLVPDSEWPELMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360
    |||||||
DB 301 NEGPTEFLRCCFDPAFLVPDSEWPELMRKLGIMDNEIKYAKAEAGHRDTLYTMLIKW 360

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QY 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411
|||||
Db 361 VNKTGRDASVHTLLDALLETGERLAKOKIEDHLLSSGKFMYLEGNADSAXS 411

RESULT 14
ID AAM93576 standard; Protein; 411 AA.
X AC AAM93576.
X XX
X DT 18-JUN-1999 (first entry)
X DE Human hAPO8 protein.
X KM Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
X KM developmental abnormality; gestational abnormality; prostate cancer;
X KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
X KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
X KM apoptosis; human.
X OS Homo sapiens.
X PN WO9911791-A2.
X PD 11-MAR-1999.
X PF 04-SEP-1998; 98WO-US18393.
X PR 05-SEP-1997; 97US-0924634.
X PA (UNIM) UNIV WASHINGTON.
X PI Chaudhary PM;
X DR WPI; 1999-205191/17.
X DR N-PDB; AAX23410.
X PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
X PT useful for diagnosis and treatment of prostate cancer and
X PT developmental or gestational abnormalities
X PS Claim 19; Fig 2; 156pp; English.

CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
X CC
X XX

SQ Sequence 411 AA;
Query Match 99.7%; Score :163; DB 20; Length 411;
Best Local Similarity 99.5%; Pred. No. 7.2e-178;
Matches 409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEORGNAPAPASGARRHGPGPREAR(ARPGLRVPTLVVAVALLVSAESALITQOD 60

Db 1 MEORGNAPAPASGARRHGPGPREAR(ARPGLRVPTLVVAVALLVSAESALITQOD 60
|||||
QY 61 LAPQGRAPQOKRSSSEBICPPGHHISEGRCISCKYGODYSTHWNDLFCLRCTRCD 120
|||||
Db 61 LAPQGRAPQOKRSSSEBICPPGHHISEGRCISCKYGODYSTHWNDLFCLRCTRCD 120
|||||
QY 121 SGVEELSPCTTNTNTYCCQCEBGFREDESPEMCRKCRTCGPRGMVVGCTPMSDIECVH 180
|||||
Db 121 SGVEELSPCTTNTNTYCCQCEBGFREDESPEMCRKCRTCGPRGMVVGCTPMSDIECVH 180
|||||
QY 181 KESGIIIGVTAAVVLAIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDRSSQRGARD 240
|||||
Db 181 KESGIIIGVTAAVVLAIVAFVCKSLMKKVLPLYLKGICSGGGDPERVDRSSQRGARD 240
|||||
QY 241 NVNLEIVSILOPVOVEQMEVQEPAPPTGVNMLSGESHLLEPAPAEESQRRLLVPA 300
|||||
Db 241 NVNLEIVSILOPVOVEQMEVQEPAPPTGVNMLSGESHLLEPAPAEESQRRLLVPA 300
|||||
QY 301 NEGDPETLROCFDDPADLVFPDWSPELMRKGLGMONEIKVAKAEAGHRDTLYTMLIKW 360
|||||
Db 301 NEGDPETLROCFDDPADLVFPDWSPELMRKGLGMONEIKVAKAEAGHRDTLYTMLIKW 360
|||||

RESULT 15
ID AAY00932 standard; Protein; 411 AA.
X AC AAY00932.
X XX
X DT 02-JUN-1999 (first entry)
X DE Human DR5 protein sequence.
X XX
X KM Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;
X KM autoimmune disease; viral infection; degenerative disorder;
X KM amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;
X KM cerebellar degeneration; myelodysplastic syndrome.
X OS Homo sapiens.
X PN WO9909165-A1.
X PD 25-FEB-1999.
X PF 14-AUG-1998; 98WO-US16945.
X PR 15-AUG-1997; 97US-0055906.
X PA (IDUN-) IDUN PHARM INC.
X PI Alnemir ES;
X DR WPI; 1999-181035/15.
X DR N-PDB; AAX27279.
X PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor
X PT protein - useful in for screening for (ant)agonists that modulate
X PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins
X XX
X PS Claim 16; Page 58-60; 71pp; English.

CC This sequence is the human TRAIL receptor DR5 of the invention. An
CC antibody against the TRAIL receptors is useful for detecting mammalian
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.
CC (ant)agonists identified by the assay are useful for modulating the
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis
CC related conditions which are treated in this way, include cancer

